

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 08:19:55 ; Search time 24 Seconds

(without alignments)
560.261 Million cell updates/sec

Title: US-09-775-964-5

Perfect score: 2398

Sequence: 1 PTDLFTNIGPDNMTWAP.....LVTLPNHLGPELDVPST 457

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

otal number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 2257 | 94.1 | 432 | 1 | US-07-959-369-8 |
| 3 | 2257 | 94.1 | 432 | 2 | US-08-836-854-20 |
| 4 | 2257 | 94.1 | 432 | 1 | US-09-366-009-4 |
| 5 | 2254 | 94.0 | 432 | 1 | US-07-959-369-9 |
| 6 | 1536.5 | 64.1 | 574 | 2 | US-08-836-854-21 |
| 7 | 1536.5 | 64.1 | 574 | 4 | US-09-463-296-1 |
| 8 | 1537 | 63.7 | 489 | 4 | US-09-366-009-24 |
| 9 | 1537 | 63.7 | 489 | 1 | US-09-366-009-8 |
| 10 | 1499 | 62.5 | 2231 | 1 | US-08-153-799-16 |
| 11 | 1485.5 | 61.9 | 302 | 2 | US-08-836-854-5 |
| 12 | 1485.5 | 61.9 | 302 | 4 | US-09-366-009-29 |
| 13 | 1474 | 61.5 | 2324 | 1 | US-08-283-857-1 |
| 14 | 1474 | 61.5 | 2324 | 6 | PCT-US95-09819-1 |
| 15 | 1474 | 61.5 | 2327 | 5 | 5455158-1 |
| 16 | 1474 | 61.5 | 2386 | 2 | US-09-016-366A-12 |
| 17 | 1474 | 61.5 | 2446 | 2 | US-08-551-356-2 |
| 18 | 1474 | 61.5 | 2446 | 5 | PCT-US93-12687-2 |
| 19 | 1463.5 | 61.0 | 472 | 4 | US-09-366-009-21 |
| 20 | 1463.5 | 61.0 | 549 | 4 | US-08-836-854-11 |
| 21 | 1463.5 | 61.0 | 549 | 4 | US-09-366-009-23 |
| 22 | 1455 | 60.7 | 422 | 2 | US-08-836-854-12 |
| 23 | 1454 | 60.6 | 826 | 4 | US-09-366-009-14 |
| 24 | 1453 | 60.6 | 446 | 2 | US-08-836-854-15 |
| 25 | 1450 | 60.4 | 332 | 2 | US-08-836-854-13 |
| 26 | 1448.5 | 60.4 | 464 | 2 | US-08-836-854-19 |
| 27 | 1448.5 | 60.4 | 464 | 4 | US-09-366-009-7 |

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| 28 | 1447.5 | 60.4 | 474 | 2 | US-08-836-854-9 | Sequence 9, Appl |
| 29 | 1447 | 60.3 | 368 | 2 | US-08-836-854-17 | Sequence 17, Appl |
| 30 | 1442 | 60.1 | 341 | 2 | US-08-836-854-14 | Sequence 14, Appl |
| 31 | 1442 | 60.1 | 367 | 2 | US-08-836-854-18 | Sequence 18, Appl |
| 32 | 1442 | 60.1 | 457 | 4 | US-08-836-854-16 | Sequence 16, Appl |
| 33 | 1442 | 60.1 | 457 | 4 | US-09-366-009-22 | Sequence 22, Appl |
| 34 | 1437 | 59.9 | 277 | 1 | US-07-959-369-3 | Sequence 3, Appl |
| 35 | 1437 | 59.9 | 279 | 1 | US-07-959-369-11 | Sequence 11, Appl |
| 36 | 1437 | 59.9 | 279 | 2 | US-08-836-854-8 | Sequence 8, Appl |
| 37 | 1437 | 59.9 | 281 | 1 | US-07-959-369-4 | Sequence 4, Appl |
| 38 | 1437 | 59.9 | 283 | 1 | US-07-959-369-13 | Sequence 13, Appl |
| 39 | 1437 | 59.9 | 283 | 2 | US-08-836-854-7 | Sequence 7, Appl |
| 40 | 1437 | 59.9 | 383 | 1 | US-07-959-369-5 | Sequence 5, Appl |
| 41 | 1437 | 59.9 | 385 | 1 | US-07-959-369-14 | Sequence 14, Appl |
| 42 | 1437 | 59.9 | 385 | 2 | US-08-836-854-10 | Sequence 10, Appl |
| 43 | 1437 | 59.9 | 491 | 1 | US-07-804-224-2 | Sequence 2, Appl |
| 44 | 1437 | 59.9 | 491 | 5 | PCT-US92-10511-2 | Sequence 2, Appl |
| 45 | 1437 | 59.9 | 1336 | 2 | US-08-551-356-6 | Sequence 6, Appl |

ALIGNMENTS

RESULT 1
US-09-366-009-5
; Sequence 5, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Yeno, Takashi
; Koyama, No. 6426042uluo
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977,6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: Linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-09-366-009-5

Query Match 100.0%; Score 2398; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 8.8e-172;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 PGTEYVSVSSVEQHESTPLRGROKGTGDSPTGIDFSDTTANSFTVHWIAPRATTIGYR 120
QY 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGRESPLLLIGOSTVSD 180
DB 121 IRHHPHSGRPREDRVPHSRNSITLTNLTGTEYVSVIALNGRESPLLLIGOSTVSD 180
QY 181 VPRDLEVVAATPSSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
DB 181 VPRDLEVVAATPSSLISMDAPAVTVRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
QY 241 PGVDYTTVYAVVGRGDSPPASSKPSISINRTETIDKPSMAGSITTLPALPEDGSGAFPP 300
DB 241 PGVDYTTVYAVVGRGDSPPASSKPSISINRTETIDKPSMAGSITTLPALPEDGSGAFPP 300
QY 301 GHRKDPKRLCYCKNGGFLRIHPDGRVDGVRKSDPHIKLOAEERGVASIKVCANRYL 360
DB 301 GHRKDPKRLCYCKNGGFLRIHPDGRVDGVRKSDPHIKLOAEERGVASIKVCANRYL 360
QY 361 AMKEDGLASKKCTDCECFEERLESNNYNTYRSKRTSMYVALKRTGOYKLGSKTGPQ 420
DB 361 AMKEDGLASKKCTDCECFEERLESNNYNTYRSKRTSMYVALKRTGOYKLGSKTGPQ 420
QY 421 KATLFLPMSAASDELPOJLVTLPHPNLGPELIDVPEST 457
DB 421 KATLFLPMSAASDELPOJLVTLPHPNLGPELIDVPEST 457

RESULT 2
US-07-959-369-8
Sequence 8, Application US/07959369
Patent No. 5302701
GENERAL INFORMATION:
APPLICANT: Higetaka HASHI et al.
TITLE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,369
FILING DATE: 19921013
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marien M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
HYPOHETICAL:
FRAGMENT TYPE:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-8

Query Match 94.1%; Score 2257; DB 1; Length 432;
Best Local Similarity 99.8%; Pred. No. 2.9e-161;
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 241 PGVDYTTVYAVVGRGDSPPASSKPSISINRTETIDKPSMAGSITTLPALPEDGSGAFPP 300

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DB 301 GHFKDPKRLCYCKNGGFFLRHPDGRVDGVRKESDPHIKLOLAEBRGVVSIKGVCANRYL 360
QY 361 AMKEDGRLASKCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420
DB 361 AMKEDGRLASKCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420
QY 421 KALFLPMSAKS 432
DB 421 KALFLPMSAKS 432

RESULT 3

US-08-836-854-20
Sequence 20, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25, 618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-20

Query Match 94.1%; Score 2257; DB 2; Length 432;
Best Local Similarity 99.8%; Pred. No. 2.9e-161;
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 PGTEYVSVSSVVEQHESTPLRGRQKTGLDSPGIDFSIDTANSFTVHWIAPRATTGGR 120

QY 121 IRHHPEHSGRPREDRVPHSRNSITLTNLPGETEYVSVIALNGREESPLLIGQOSTVSD 180
DB 121 IRHHPEHSGRPREDRVPHSRNSITLTNLPGETEYVSVIALNGREESPLLIGQOSTVSD 180
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DB 181 VPRDLEVAATPTSLISMDAPAVTVRYRITTYGETGNSPVQEFVPGSKSTATTISGLK 240
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DB 301 GHFKDPKRLCYCKNGGFFLRHPDGRVDGVRKESDPHIKLOLAEBRGVVSIKGVCANRYL 360
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DB 361 AMKEDGRLASKCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGQYKLSKTGPQ 420
QY 421 KALFLPMSAKS 432
DB 421 KALFLPMSAKS 432

RESULT 4

US-09-366-009-4
Sequence 4, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Ueno, Takashi
APPLICANT: Koyama, No. 6426042uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid

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STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-366-009-4

Query Match
Best Local Similarity 94.1%; Score 2257; DB 4; Length 432;
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 PTDLRFNTIGPDMRYMAPPSPIDLTNFIYRSPVKNEDVAELISPSDNVAVLTNLL 60
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DB 61 PGTEYVSVSSVYEOHESTPLRGOKTGIDSPGIDFSDITANSFTVHWIAPRATTGXR 120
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DB 121 IRHHPHSGRPREDRYPHSRNSITLTNLTGTEYVSVIALNGRRESPLLIGQSTVSD 180
QY 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFYVPGSKSTATISGLK 240
DB 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFYVPGSKSTATISGLK 240
QY 241 PGVDYTTVYAVTGRGSPASSKPSISINYRTETIDKPSMAAGSTITLPALPEDGSGAFP 300
DB 241 PGVDYTTVYAVTGRGSPASSKPSISINYRTETIDKPSMAAGSTITLPALPEDGSGAFP 300
QY 301 GHFNDPKRLCYCKNGCFELRHPDGRVGVREKSDPHIKLOAEERGVVSIKGCANRYL 360
DB 301 GHFNDPKRLCYCKNGCFELRHPDGRVGVREKSDPHIKLOAEERGVVSIKGCANRYL 360
QY 361 AMKEDGRLASKCVTDCEFFERLESNNYNTYRSKXTSWYVALKRGQVYKSGKTGPGQ 420
DB 361 AMKEDGRLASKCVTDCEFFERLESNNYNTYRSKXTSWYVALKRGQVYKSGKTGPGQ 420
QY 421 KATIFLPMASAS 432
DB 421 KATIFLPMASAS 432

RESULT 5
US-07-959-369-9
Sequence 9, Application US/07959369
Patent No. 5302701
GENERAL INFORMATION:
APPLICANT: Higetaka HASHI et al.
TITLE OF INVENTION: No. 5302701el Functional Polypeptide
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959, 369
FILING DATE: 19921013
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mairen M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
```

```
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
MOLECULE TYPE: polypeptide
TOPOLOGY: linear
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-9

Query Match
Best Local Similarity 94.0%; Score 2254; DB 1; Length 432;
Matches 430; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 PTDLRFNTIGPDMRYMAPPSPIDLTNFIYRSPVKNEDVAELISPSDNVAVLTNLL 60
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DB 61 PGTEYVSVSSVYEOHESTPLRGOKTGIDSPGIDFSDITANSFTVHWIAPRATTGXR 120
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DB 121 IRHHPHSGRPREDRYPHSRNSITLTNLTGTEYVSVIALNGRRESPLLIGQSTVSD 180
QY 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFYVPGSKSTATISGLK 240
DB 181 VPRDLEVVAATPTSLISMDAPAVTVRYRITYGETGNSPVQEFYVPGSKSTATISGLK 240
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DB 241 PGVDYTTVYAVTGRGSPASSKPSISINYRTETIDKPSMAAGSTITLPALPEDGSGAFP 300
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Db 241 PGVDYTIYVAVTGRGDSPPASSKPIISINRYTEIDKPSMAAGSITTLPALPEDGSGAEP 300
Qy 301 GHFDPKRLCYCKNGGFFLRHPDGRVDGVRKESDPHIKLOAEERGVVSTIKGVANRYL 360
Db 301 GHFDPKRLCYCKNGGFFLRHPDGRVDGVRKESDPHIKLOAEERGVVSTIKGVANRYL 360
Qy 361 AMKEDGRLLASCKVYDECFEERLESNNYNTYRSRKYTSWYVALKRTQYKLGSKTGFQ 420
Db 361 AMKEDGRLLASCKVYDECFEERLESNNYNTYRSRKYTSWYVALKRTQYKLGSKTGFQ 420
Qy 421 KAILFLPMASAS 432
Db 421 KAILFLPMASAS 432

RESULT 6
US-08-836-854-21
; Sequence 21, Application US/08836854
; Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836, 854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 574 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-21

Query Match 64.1%; Score 1536.5; DB 2; Length 574;
Best Local Similarity 58.0%; Pred. No. 3.4e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

Qy 1 PTDLFTNIGPDTMRYTMAPPSIDLTNLFVRYSPVKNEDVAAELISPSDNAVVLTNLL 60
Db 1 PTDLFTNIGPDTMRYTMAPPSIDLTNLFVRYSPVKNEDVAAELISPSDNAVVLTNLL 60
Qy 61 PGTETVVSASSYVEQHESTPLRGKRTGLDSTGIDFSIDITANSFTVHWIAPRATITGVR 120
Db 61 PGTETVVSASSYVEQHESTPLRGKRTGLDSTGIDFSIDITANSFTVHWIAPRATITGVR 120

Db 61 PGTETVVSASSYVEQHESTPLRGKRTGLDSTGIDFSIDITANSFTVHWIAPRATITGVR 120
Qy 121 IRHHEHSGRPREDRVPHSRNSITLTNLTPTETEVVSVALANGREESPLLGOOSTVSD 180
Db 121 IRHHEHSGRPREDRVPHSRNSITLTNLTPTETEVVSVALANGREESPLLGOOSTVSD 180
Qy 181 VPRDLEVAATPTSLIISMDAPAVTVRYRYRTYGETGGSNPOEFTVPGSKSTATISGLK 240
Db 181 VPRDLEVAATPTSLIISMDAPAVTVRYRYRTYGETGGSNPOEFTVPGSKSTATISGLK 240
Qy 241 PGVDYTIYVAVTGRGDSPPASSKPIISINRYTEIDKPSMAAGSITTL--PALPEDGSGA 297
Db 241 PGVDYTIYVAVTGRGDSPPASSKPIISINRYTEIDKPSMAAPAPDLPKFTQVPTSLAQW 300
Qy 298 FPGHFKDPKRLCYCKNGGFFLRHPDGRVDGVRKESDPHIKLOAEERGVVSTIKGVAN 357
Db 301 TPNP-----VOLTGRRVTP-----KEKTGPKETINLAPDSSSVVSGLMAT 344
Qy 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
Db 345 KVEVSVALKD---TLTSRPAQGVYTTLENSPRRARVTDATETTTISMTKETETITG 401
Qy 379 FFEERLESNNYNTYRS-----RKYT----- 398
Db 402 PGVDAPVANGQTPIQRTIKPDVSYTTGLQPTDYKIITYLTLDNMASSPVVIDASTAI 461
Qy 399 -----SWYVALKRTGY-----KLGSK-----TG- 417
Db 462 DAPSNLRELTATPNSLIVSWOPPARITGYIIRKPKSPPREVVPRPPGVTEATITGL 521
Qy 418 -PGOKAIFL-----PM--SAASDELPLQVTLPHPNLHGEILDVPST 457
Db 522 EPGETYTIYVALKNNQKSEPLIGRKKTDLPQVTLPHPNLHGEILDVPST 574

RESULT 7
US-09-463-296-1
; Sequence 1, Application US/09463296
; Patent No. 6287864
GENERAL INFORMATION:
APPLICANT: BAGNIS, Claude
APPLICANT: IMBERT, Anne-Marie
APPLICANT: MANNONI, Patrice
TITLE OF INVENTION: GENE TRANSFER METHOD WITH THE USE OF SERUM-FREE MEDIUM
FILE REFERENCE: BAGNIS-1
CURRENT APPLICATION NUMBER: US/09/463, 296
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/JP98/03173
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: JP 196772/1997
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-09-463-296-1

Query Match 64.1%; Score 1536.5; DB 4; Length 574;
Best Local Similarity 58.0%; Pred. No. 3.4e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

Qy 1 PTDLFTNIGPDTMRYTMAPPSIDLTNLFVRYSPVKNEDVAAELISPSDNAVVLTNLL 60
Db 1 PTDLFTNIGPDTMRYTMAPPSIDLTNLFVRYSPVKNEDVAAELISPSDNAVVLTNLL 60
Qy 61 PGTETVVSASSYVEQHESTPLRGKRTGLDSTGIDFSIDITANSFTVHWIAPRATITGVR 120
Db 61 PGTETVVSASSYVEQHESTPLRGKRTGLDSTGIDFSIDITANSFTVHWIAPRATITGVR 120
Qy 121 IRHHEHSGRPREDRVPHSRNSITLTNLTPTETEVVSVALANGREESPLLGOOSTVSD 180
Db 121 IRHHEHSGRPREDRVPHSRNSITLTNLTPTETEVVSVALANGREESPLLGOOSTVSD 180

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Db 121 IRHHPHFGSRPREDRVPHSRNSITLNLTPGTEYVSVIALNGREESPLLIGQSTVSD 180
QY 181 VPRDLEVVAAVPTPTSLISMDAPAVTVRYRYITVGETGNSPVQETVPQSGSTATISGLK 240
Db 181 VPRDLEVVAAVPTPTSLISMDAPAVTVRYRYITVGETGNSPVQETVPQSGSTATISGLK 240
QY 241 PGVDITTYVAVTGRDSDPASKPISINRTETIDKPSMAAGSITTL---PALPEDGSGA 297
Db 241 PGVDITTYVAVTGRDSDPASKPISINRTETIDKPSMAAGSITTL---PALPEDGSGA 297
QY 298 FPGHFKDPKRLYCKNGGFFLRHPDGRVGVREKSDPHIKLOLAERGVSIGVCAN 357
Db 298 FPGHFKDPKRLYCKNGGFFLRHPDGRVGVREKSDPHIKLOLAERGVSIGVCAN 357
QY 301 TFPN-----VOLTGRVAVTTP-----KEKTGPKMEINLADSSVYVSGLMVAT 344
Db 301 TFPN-----VOLTGRVAVTTP-----KEKTGPKMEINLADSSVYVSGLMVAT 344
QY 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
Db 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
QY 345 KEVSVYALKD---TLTSRAGGVTTLENVSPRRARVTDATETTTITTSWRTKETITIG 401
Db 345 KEVSVYALKD---TLTSRAGGVTTLENVSPRRARVTDATETTTITTSWRTKETITIG 401
QY 379 FFEERLESNNVNTYRS-----RKYT----- 398
Db 379 FFEERLESNNVNTYRS-----RKYT----- 398
QY 402 FOYDAVPANGQPTPIORTIKPDVRSYTTITGLQPGTDYKIYLTLDNARSSPVVIDASTAI 461
Db 402 FOYDAVPANGQPTPIORTIKPDVRSYTTITGLQPGTDYKIYLTLDNARSSPVVIDASTAI 461
QY 462 DAPSNLFLATTPNSLWSQPPRARITGYIIRKPKGSPREVPVPRPGVTEATITGL 521
Db 462 DAPSNLFLATTPNSLWSQPPRARITGYIIRKPKGSPREVPVPRPGVTEATITGL 521
QY 418 -PGOKAIFL-----PM--SASDELPLQVTLPHPNLHGPELIDVPST 457
Db 418 -PGOKAIFL-----PM--SASDELPLQVTLPHPNLHGPELIDVPST 457
QY 522 EPGETEYIVIALKNOKSEPLIGRKKTDELPLQVTLPHPNLHGPELIDVPST 574
Db 522 EPGETEYIVIALKNOKSEPLIGRKKTDELPLQVTLPHPNLHGPELIDVPST 574

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RESULT 8

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US-09-366-009-24
; Sequence 24, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:

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```

APPLICANT: Asada, Kiyozo
            Umori, Takashi
            Koyama, No. 642604Zuto
            Hashino, Kimikazu
            Kato, Ikunoshin

```

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TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977,6507P
TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-366-009-24

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Query Match      64.1% Score 1536.5; DB 4; Length 574;
Best Local Similarity 58.0%; Pred. No. 3.4e-107;
Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

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QY 1 PTDLRTNIGPPTMYVMAAPPSIDLTFNLVRYSPVKNEDVYAEUSISPSDNVAVLNL 60
Db 1 PTDLRTNIGPPTMYVMAAPPSIDLTFNLVRYSPVKNEDVYAEUSISPSDNVAVLNL 60
QY 61 PCTEVYVSVSYEHESTPLRGKQTGLDSDITANSFTVHVIARATITGYR 120
Db 61 PCTEVYVSVSYEHESTPLRGKQTGLDSDITANSFTVHVIARATITGYR 120
QY 121 IRHHPHFGSRPREDRVPHSRNSITLNLTPGTEYVSVIALNGREESPLLIGQSTVSD 180
Db 121 IRHHPHFGSRPREDRVPHSRNSITLNLTPGTEYVSVIALNGREESPLLIGQSTVSD 180
QY 181 VPRDLEVVAAVPTPTSLISMDAPAVTVRYRYITVGETGNSPVQETVPQSGSTATISGLK 240
Db 181 VPRDLEVVAAVPTPTSLISMDAPAVTVRYRYITVGETGNSPVQETVPQSGSTATISGLK 240
QY 241 PGVDITTYVAVTGRDSDPASKPISINRTETIDKPSMAAGSITTL---PALPEDGSGA 297
Db 241 PGVDITTYVAVTGRDSDPASKPISINRTETIDKPSMAAGSITTL---PALPEDGSGA 297
QY 298 FPGHFKDPKRLYCKNGGFFLRHPDGRVGVREKSDPHIKLOLAERGVSIGVCAN 357
Db 298 FPGHFKDPKRLYCKNGGFFLRHPDGRVGVREKSDPHIKLOLAERGVSIGVCAN 357
QY 301 TFPN-----VOLTGRVAVTTP-----KEKTGPKMEINLADSSVYVSGLMVAT 344
Db 301 TFPN-----VOLTGRVAVTTP-----KEKTGPKMEINLADSSVYVSGLMVAT 344
QY 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
Db 358 RY-----LAMKEDGRLLASK-----CVTDEC----- 378
QY 345 KEVSVYALKD---TLTSRAGGVTTLENVSPRRARVTDATETTTITTSWRTKETITIG 401
Db 345 KEVSVYALKD---TLTSRAGGVTTLENVSPRRARVTDATETTTITTSWRTKETITIG 401
QY 379 FFEERLESNNVNTYRS-----RKYT----- 398
Db 379 FFEERLESNNVNTYRS-----RKYT----- 398
QY 402 FOYDAVPANGQPTPIORTIKPDVRSYTTITGLQPGTDYKIYLTLDNARSSPVVIDASTAI 461
Db 402 FOYDAVPANGQPTPIORTIKPDVRSYTTITGLQPGTDYKIYLTLDNARSSPVVIDASTAI 461
QY 462 DAPSNLFLATTPNSLWSQPPRARITGYIIRKPKGSPREVPVPRPGVTEATITGL 521
Db 462 DAPSNLFLATTPNSLWSQPPRARITGYIIRKPKGSPREVPVPRPGVTEATITGL 521
QY 418 -PGOKAIFL-----PM--SASDELPLQVTLPHPNLHGPELIDVPST 457
Db 418 -PGOKAIFL-----PM--SASDELPLQVTLPHPNLHGPELIDVPST 457
QY 522 EPGETEYIVIALKNOKSEPLIGRKKTDELPLQVTLPHPNLHGPELIDVPST 574
Db 522 EPGETEYIVIALKNOKSEPLIGRKKTDELPLQVTLPHPNLHGPELIDVPST 574

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RESULT 9

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US-09-366-009-8
; Sequence 8, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:

```

```

APPLICANT: Asada, Kiyozo
            Umori, Takashi
            Koyama, No. 642604Zuto
            Hashino, Kimikazu
            Kato, Ikunoshin

```

```

TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>

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STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-366-009-8
Query Match 63.7%; Score 1527; DB 4; Length 489;
Best Local Similarity 65.5%; Pred. No. 1.4e-106;
Matches 342; Conservative 7; Mismatches 75; Indels 98; Gaps 11;
QY 1 PTDLFTNIGPDTMRYTMAAPPSSIDLTLNPLVRSYPKNEEDVAELISPSDNAVVLTNLL 60
DB 1 PTDLFTNIGPDTMRYTMAAPPSSIDLTLNPLVRSYPKNEEDVAELISPSDNAVVLTNLL 60
QY 61 PETEVYVSVSYEQHESTPLRGROKTDGDSPTGIDFSDTANSFTVMIAPRATITGYR 120
b 61 PETEVYVSVSYEQHESTPLRGROKTDGDSPTGIDFSDTANSFTVMIAPRATITGYR 120
QY 121 IHHHEHFGRRPDRVPHSRNSITLTNTPTGETYVVSVALNGRESPLLIQOSTVSD 180
DB 121 IHHHEHFGRRPDRVPHSRNSITLTNTPTGETYVVSVALNGRESPLLIQOSTVSD 180
QY 181 VPRDLEVVAATPSTLLISMDAPAVTRYRYTYGETGNSPYOEFTVPGSKSTATISGLK 240
DB 181 VPRDLEVVAATPSTLLISMDAPAVTRYRYTYGETGNSPYOEFTVPGSKSTATISGLK 240
QY 241 PGVDYITIVYAVTGRDPSASSKPSISINRYTEIDKPSMA-AGSITTLPALPEDGGSG-- 296
DB 241 PGVDYITIVYAVTGRDPSASSKPSISINRYTEIDKPSMA-AGSITTLPALPEDGGSG-- 296
QY 297 -----AFPGHF-----KDKRLYCKNG-----GFLRLRH 321
DB 301 DMGIKGRKEIGPPGREGDEGEPGRRGGPGNDGPGPLCPGEKGLGVPGYGRGOG 360
QY 322 PDGRVD-----GVREKSDPHIKLQLAQEERGVAIVKVCANRYLAME--- 364
DB 361 PGSGIGFPFPGANGKGRGTGPKGPR-----GGRGPIGPKRERPRGTGKPGRK 413
QY 365 -----DGRLLASKCYTDECFFPERLESNNYNTYRSKRYTSWYVALKRTGOYKLGSTGPG 419
DB 414 GNSGGDGPAGPG-----ERGNCGPGP-----TG--FPGKGPBG 447

QY 420 QKALFLP---MSASDELPOLVTLPHPLHGPETLDVST 457
DB 448 PPKGDLPGHPGORGASDELPOLVTLPHPLHGPETLDVST 489
RESULT 10
US-08-153-799-16
Sequence 16, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2231 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Protein
LOCATION: 1..2231
OTHER INFORMATION: /note= "Human fibronectin"
US-08-153-799-16
Query Match 62.5%; Score 1499; DB 1; Length 2231;
Best Local Similarity 51.4%; Pred. No. 1.3e-103;
Matches 346; Conservative 31; Mismatches 64; Indels 232; Gaps 17;
QY 1 PTDLFTNIGPDTMRYTMAAPPSSIDLTLNPLVRSYPKNEEDVAELISPSDNAVVLTNLL 60
DB 1239 PTDLFTNIGPDTMRYTMAAPPSSIDLTLNPLVRSYPKNEEDVAELISPSDNAVVLTNLL 1298

61 PCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 120
DB PCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 1358
121 IRHHEHESGRREDVRPHSRNSITLNTLFTPCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 180
1359 IRHHEHESGRREDVRPHSRNSITLNTLFTPCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 1418
181 VRDLLEVAATPTSLISIDAPAVTVRYRITRYGEGNSPVQOEFTVPSKSTATISGLK 240
1419 VRDLLEVAATPTSLISIDAPAVTVRYRITRYGEGNSPVQOEFTVPSKSTATISGLK 1478
241 PGVDYTTIYVAVTGRGDSVASSKSPISINRTEDIKPMA-----AGSTITLFA----- 288
1479 PGVDYTTIYVAVTGRGDSVASSKSPISINRTEDIKPMA-----AGSTITLFA----- 1538
289 -----LPEDGSGAFPPGHRKDKP-----RLYCKN----- 313
1539 TGYRVTTTPKNG-----PGPKTKTAGPDQTEMTIEGLQPTVEYVSVYAOQPSGESOP 1592
314 -----GGFFLIRHPDGRVDGVRKSDPHI 337
1593 LVQVATVTPAPTDLKFQVPTSLSAQWTPPDVOLTGYRVAVTP-----KOKTGPMK 1645
338 KLOAEERGVSIGVCANRY-----LAKKEDGRLLASK-----CVT 375
1646 EINIAPDSSVSVGLMVAATKVEYSVYALKD-----TLTSRPAQGVVTLLENVSPRRARVT 1702
376 DEC-----PFERLESNNNTYRS-----RKYT----- 398
1703 DATETTTISMTKETETITGFOVDVAVPANGOTPIQRTIKPDVRSYTIINGLOPCTDYKYL 1762
399 -----SNVYALKRTQY-----KLGSK 415
1763 YTLNDAASSPVVIDASTAIDAPASNRLATTPNSLSVWOPPARITTYITIKYKPGSP 1822
416 -----TG-----PGOKAILFL-----PM-----SASDELPLQVLTLPHP 444
1823 PREVYPRPVGTATITGLEPGETTYIVALKNNKSEPLIGRKTDELQVLTLPHP 1882
445 NLHGEILDPST 457
1883 NLHGEILDPST 1895

RESULT 11
US-08-836-854-5
Sequence 5, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hiroyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSCRIPTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Broadway and Neilmark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/J95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Broadway, Roger L.
REFERENCE NUMBER: 25, 618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-5

Query Match 61.9%; Score 1485.5; DB 2; Length 302;
Best Local Similarity 66.1%; Pred. No. 9.6e-104;
Matches 302; Conservative 0; Mismatches 0; Indels 155; Gaps 1;

1 PDLRFTNIGPTMTVMAPEPSIDLTNPLVRYSPVKNEDVAVELTSPSDNAVLTNLL 60
1 PDLRFTNIGPTMTVMAPEPSIDLTNPLVRYSPVKNEDVAVELTSPSDNAVLTNLL 60
61 PCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 120
61 PCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 120
121 IRHHEHESGRREDVRPHSRNSITLNTLFTPCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 180
121 IRHHEHESGRREDVRPHSRNSITLNTLFTPCTEYVSVSSVYEOHESTPLRGROKGTGDSPTGIDFSDITANSEFTVHVIAPRATITGYR 180
181 VRDLLEVAATPTSLISIDAPAVTVRYRITRYGEGNSPVQOEFTVPSKSTATISGLK 240
181 VRDLLEVAATPTSLISIDAPAVTVRYRITRYGEGNSPVQOEFTVPSKSTATISGLK 240
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241 PGVDYTTIYVAVTGRGDSVASSKSPISINRTEDIKPMAAGSITLPLALPEDGSGAAPP 300
241 PGVDYTTIYVAVTGRGDSVASSKSPISINRTEDIKPMAAGSITLPLALPEDGSGAAPP 300
301 GHKDPKRLYCKNGFFLIRHPDGRVDGVRKSDPHIKLOAEERGVSIGVCANRYL 360
277 ----- 276
361 AKKEDGRLLASKCVIDECEFFERLESNNNTYRSRKYTSWYVYALKRTQYKLGSKTGPQ 420
277 ----- 276
421 KAILFLPMSASDELPLQVLTLPHPNLHGEILDPST 457
277 -----SDELPLQVLTLPHPNLHGEILDPST 302

RESULT 12
US-09-366-009-29
Sequence 29, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Koyama, No. 6426042uto
APPLICANT: Hashino, Kimikazu
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-366-009-29

Query Match 61.9%; Score 1485.5; DB 4; Length 302;
Best Local Similarity 66.1%; Pred. No. 9.6e-104;
Matches 302; Conservative 0; Mismatches 0; Indels 155; Gaps 1;

QY 1 PTDLFTNIGPDTMRTAAPPSSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
DB 1 PTDLFTNIGPDTMRTAAPPSSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
QY 61 PGTETVVSVSVEQHESTPLRGROKGTGLDPTGIDFSITANSFTVHMIARATITGYR 120
DB 61 PGTETVVSVSVEQHESTPLRGROKGTGLDPTGIDFSITANSFTVHMIARATITGYR 120
QY 121 IRHHEHFSGRPREDRVPHSRNSITLNLTPGTETVVSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHFSGRPREDRVPHSRNSITLNLTPGTETVVSIVALNGREESPLLIGQOSTVSD 180
QY 181 VPRDLEVAAPTSLISMDAPAVTVRYRYRITYGETGNSPQOETVPESKSTATISGLK 240
DB 181 VPRDLEVAAPTSLISMDAPAVTVRYRYRITYGETGNSPQOETVPESKSTATISGLK 240
QY 241 PGVDITIVYAVTGRGDSPASSKPSISYRTEIDKPSMAAGSITLPLALPEDGSGAAPP 300
DB 241 PGVDITIVYAVTGRGDSPASSKPSISYRTEIDKPSMAAGSITLPLALPEDGSGAAPP 300
QY 301 GHFKDPKRLYCKNGGFLRIHPDGVNDGVRKSDPHIKLQLOAERGVVSIKVCANRYL 360
DB 277 ----- 276
QY 361 AMKEDGRLLASKCTVDECFERLESNMYNTYRSRKITSWYALKRTGYKLGSKTGRCQ 420
DB 277 ----- 276
QY 421 KALFLPMSAASDELPLQVTLPHPNLHGPEILDVPSST 457
DB 277 ----- 276

DB 277 -----SDELPLQVTLPHPNLHGPEILDVPSST 302

RESULT 13
US-08-283-857-1
Sequence 1, Application US/08283857
Patent No. 5792742
GENERAL INFORMATION:
APPLICANT: GOLD, Leslie I.
APPLICANT: ROSTAGNO, Agueda A.
APPLICANT: BARON, Martin
APPLICANT: CAMPBELL, Iain D.
APPLICANT: WILLIAMS, Michael, J.
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,857
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/714,134
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOLD-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2324 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-283-857-1

Query Match 61.5%; Score 1474; DB 1; Length 2324;
Best Local Similarity 46.8%; Pred. No. 9.9e-102;
Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

QY 1 PTDLFTNIGPDTMRTAAPPSSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
DB 1239 PTDLFTNIGPDTMRTAAPPSSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 1298
QY 61 PGTETVVSVSVEQHESTPLRGROKGTGLDPTGIDFSITANSFTVHMIARATITGYR 120
DB 1299 PGTETVVSVSVEQHESTPLRGROKGTGLDPTGIDFSITANSFTVHMIARATITGYR 1358
QY 121 IRHHEHFSGRPREDRVPHSRNSITLNLTPGTETVVSIVALNGREESPLLIGQOSTVSD 180
DB 1359 IRHHEHFSGRPREDRVPHSRNSITLNLTPGTETVVSIVALNGREESPLLIGQOSTVSD 1418
QY 181 VPRDLEVAAPTSLISMDAPAVTVRYRYRITYGETGNSPQOETVPESKSTATISGLK 240
DB 1419 VPRDLEVAAPTSLISMDAPAVTVRYRYRITYGETGNSPQOETVPESKSTATISGLK 1478
QY 241 PGVDITIVYAVTGRGDSPASSKPSISYRTEIDKPSMAAGSITLPLALPEDGSGAAPP 300
DB 241 PGVDITIVYAVTGRGDSPASSKPSISYRTEIDKPSMAAGSITLPLALPEDGSGAAPP 300

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Db 1479 PGVDYITIVYAVTGRGDSFASCKPISINRYTEIDKPSQMQVTDVQDINSISVKMLPSSSPV 1538
OY 279 AAGSITTLT----- 287
Db 1539 TGYRVYITPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTA 1598
OY 288 -----ALPEDGSGAAP-PGHFKDPKRL 309
Db 1599 TNDPRKGLAFTDVVDYSIKIAMESPQGVSRVRYTSSPEDGHELFAPDGEETPAEL 1658
OY 310 YCKNGV-----FELRIH-----PDGVR 326
Db 1659 QGLRGSEYTVSVVALHDMESQPLIGTOSTAIPAPDLKFTQVPTSLSAQMTFPPVQL 1718
OY 327 DGVR-----EKSDPHIKILOAEERGVSIGVCANRY-----LAMKEDGRLLASK----- 372
Db 1719 TGYRVYITPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTA 1775
OY 373 -----CVTDEC-----FFERLESNNNTYRS-----R 395
Db 1776 VVTLLENVSPRRARVDTATETTTITISWRTKETITTGFOVDAPVANGQTPIQRTIKPDVR 1835
OY 396 KYT-----SWYVA 403
Db 1836 STTIGLOPGTDYKIYLYTLNDNASSPVVIDASTAIDAPSNLRLATTPNSLWSWOP 1895
OY 404 LKRTQY-----KLGSK-----TG--PGOKAILEL-----PM- 428
Db 1896 RARITGYITIKYKPGSPREVPVPRPGVTEATITGLEGTETTYIYIALKNKQSEPLI 1955
OY 429 -SAASDELPLQVTLTPHPNLHGPEILDVST 457
Db 1956 GRKKTDELPLQVTLTPHPNLHGPEILDVST 1985

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RESULT 14

PCT-US95-09819-1

Sequence 1 Application PC/TUS9509819

GENERAL INFORMATION:

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APPLICANT:
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREFOR AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09819

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,857

FILING DATE: 01-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: GOLD-1A PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2324 amino acids

TYPE: amino acid

```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-09819-1

```

```

Query Match 61.5%; Score 1474; DB 5; Length 2324;
Best Local Similarity 46.8%; Pred No. 9,9e-102;
Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

```

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OY 1 PDLRFTNIGPPTMRVYVAPPSIDITNLFVYSPVKNEDVAELISFSDNAVLTNLL 60
Db 1239 PDLRFTNIGPPTMRVYVAPPSIDITNLFVYSPVKNEDVAELISFSDNAVLTNLL 1298
OY 61 PGTEYVSVSVYEGHESTPLRGOKTGLDSDITANSFTVHVIAPRATITGYR 120
Db 1299 PGTEYVSVSVYEGHESTPLRGOKTGLDSDITANSFTVHVIAPRATITGYR 1358
OY 121 IHHHEHESGRRERDVRPHSRNSITLNTLPGTEYVSVSVYALNGREESPLLCQOSTVSD 180
Db 1359 IHHHEHESGRRERDVRPHSRNSITLNTLPGTEYVSVSVYALNGREESPLLCQOSTVSD 1418
OY 181 VPRDLEVVAVATPTSLISMDAPAVTRYRYTYGEGNSPQOETVPGSKSTATISGLK 240
Db 1419 VPRDLEVVAVATPTSLISMDAPAVTRYRYTYGEGNSPQOETVPGSKSTATISGLK 1478
OY 241 PGVDYITIVYAVTGRGDSFASCKPISINRYTEIDKPSQMQVTDVQDINSISVKMLPSSSPV 278
Db 1479 PGVDYITIVYAVTGRGDSFASCKPISINRYTEIDKPSQMQVTDVQDINSISVKMLPSSSPV 1538
OY 279 AAGSITTLT----- 287
Db 1539 TGYRVYITPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTA 1598
OY 288 -----ALPEDGSGAAP-PGHFKDPKRL 309
Db 1599 TNDPRKGLAFTDVVDYSIKIAMESPQGVSRVRYTSSPEDGHELFAPDGEETPAEL 1658
OY 310 YCKNGV-----FELRIH-----PDGVR 326
Db 1659 QGLRGSEYTVSVVALHDMESQPLIGTOSTAIPAPDLKFTQVPTSLSAQMTFPPVQL 1718
OY 327 DGVR-----EKSDPHIKILOAEERGVSIGVCANRY-----LAMKEDGRLLASK----- 372
Db 1719 TGYRVYITPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPSGESQPLVQTA 1775
OY 373 -----CVTDEC-----FFERLESNNNTYRS-----R 395
Db 1776 VVTLLENVSPRRARVDTATETTTITISWRTKETITTGFOVDAPVANGQTPIQRTIKPDVR 1835
OY 396 KYT-----SWYVA 403
Db 1836 STTIGLOPGTDYKIYLYTLNDNASSPVVIDASTAIDAPSNLRLATTPNSLWSWOP 1895
OY 404 LKRTQY-----KLGSK-----TG--PGOKAILEL-----PM- 428
Db 1896 RARITGYITIKYKPGSPREVPVPRPGVTEATITGLEGTETTYIYIALKNKQSEPLI 1955
OY 429 -SAASDELPLQVTLTPHPNLHGPEILDVST 457
Db 1956 GRKKTDELPLQVTLTPHPNLHGPEILDVST 1985

```

RESULT 15

5455158-1

Patent No. 5455158

APPLICANT: VOGEL, TIKVA; LEVANON, AVIGDOR; WERBER, MOSHE M.;

GUY, RACHEL; PANET, AMOS

TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND

USES AND METHODS OF PRODUCING SAME

NUMBER OF SEQUENCES: 20

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/58,241

FILING DATE: 04-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 526,397

FILING DATE: 21-MAY-1990

APPLICATION NUMBER: 345,952

FILING DATE: 28-APR-1989

APPLICATION NUMBER: 291,951

FILING DATE: 29-DEC-1988

SEQ ID NO:1:

LENGTH: 2327

5455158-1

Query Match

61.5%; Score 1474; DB 6; Length 2327;

Best Local Similarity 46.8%; Pred. No. 9,9e-102;

Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

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OY 1 PTDLFTNIGPTMTVTAAPPSIDLTNLFVRSPPKNEEDVAELSPSDNAVLTNLL 60
Db 1242 PTDLFTNIGPTMTVTAAPPSIDLTNLFVRSPPKNEEDVAELSPSDNAVLTNLL 1301
OY 61 PCTEVVSVSVYEQHESTPLGRROKTGLDPTGIDFSDITANSFTVHWIAPRATTGYR 120
Db 1302 PCTEVVSVSVYEQHESTPLGRROKTGLDPTGIDFSDITANSFTVHWIAPRATTGYR 1361
OY 121 IRHHEHESGRREDVRPHSRNSITLTNLTPTGEVVSIVALNGRESPLLIGQSTVSD 180
Db 1362 IRHHEHESGRREDVRPHSRNSITLTNLTPTGEVVSIVALNGRESPLLIGQSTVSD 1421
OY 181 VPRDLEVVAATPTSLISDAPAVVRYRITYGETGNSPVOEFTVPGSKSTATISGLK 240
Db 1422 VPRDLEVVAATPTSLISDAPAVVRYRITYGETGNSPVOEFTVPGSKSTATISGLK 1481
OY 241 PCVDYTIYVAVTGRGDSPPASSKPISINRYTEIDKPS-----M 278
Db 1482 PCVDYTIYVAVTGRGDSPPASSKPISINRYTEIDKPSQMVVDVODNSISVKWLPSSPY 1541
OY 279 AAGSITTLT----- 287
Db 1542 TGYRVTTTPKNGPGPTKTAGPDQEMTIEGLQPTVEVVSVAQNPGESQPLVQTAV 1601
OY 288 -----ALPEDGGSGAFP-PGHFKDPKRL 309
Db 1602 TNIDRPKGLAFTDVDSIKIAMESPOGVSRYRVYSSPEDGIHELFPAPDGEEDTAEL 1661
OY 310 YCKNGC-----FELRIH-----PDGRV 326
Db 1662 QGLRPGSEYTVVALHDMESQPLIGTOSTAIPAPTDLKTQVPTSLSAQWTPPNVOL 1721
OY 327 DGVR-----EKSDPHIKLQLOAERGVSIRKVCANRY---LAKKEDGRLASK--- 372
Db 1722 TGYRVAVTPKEKTEGPMKEINLAPDSSSVVSGIMVATKYEVSVALKD---TLTSRPAOG 1778
OY 373 -----CVTDEC-----FFERLESNNVNTYRS-----R 395
Db 1779 VVTTLENNVSPRARAVTDATEFTTITISWRTKETITINGFOVDVAPANGQTPIQRTIKPDVR 1838
OY 396 KYT-----SWYVA 403
Db 1839 SYTTIGLOPCTDKIYLYTLNDNANSSPVYIDASTAIDAPSNIURLATTPNLSLVSWOPP 1898
OY 404 LKRTGOY-----KLGSK-----TG-PGOKAILFL-----PM- 428
Db 1899 RARITGYIIRKPKGSPPREVVPRPRPGVTEATITIGLEGTETIYVIALKNNQKSEPLI 1958
OY 429 -SAASDELQOLYTLRHPNLHGPEILDVPS 457
Db 1959 GRKKTDELQOLYTLRHPNLHGPEILDVPS 1988
```

Search completed: March 13, 2003, 09:40:27
Job time : 33 secs

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|--------------------------|-------------------|
| Protein sequence | Human fibronectin |
| Protein used in database | Human fibronectin |
| Chimeric inhibitor | Human fibronectin |
| Human polypeptide | Human fibronectin |
| Chimeric inhibitor | Human fibronectin |
| Cell adhesion substrate | Human fibronectin |
| Oligopeptide C277-1 | Human fibronectin |
| Human fibronectin | Human fibronectin |
| Human protein related | Human fibronectin |
| Human fibronectin | Human fibronectin |
| Human fibronectin | Human fibronectin |
| Human fibronectin | Human fibronectin |
| Human fibronectin | Human fibronectin |
| Novel | Human fibronectin |
| Human polypeptide | Human fibronectin |
| Human polypeptide | Human fibronectin |
| Oligopeptide CHV-1 | Human fibronectin |
| Fibronectin analog | Human fibronectin |
| Fibronectin analog | Human fibronectin |
| Chimeric inhibitor | Human fibronectin |
| Oligopeptide CH-272 | Human fibronectin |
| Human fibronectin | Human fibronectin |
| Fibronectin receptor | Human fibronectin |
| CH-286 Oligopeptide | Human fibronectin |
| Fibronectin-spacer | Human fibronectin |
| Cell adhesive and | Human fibronectin |
| EGF-fibronectin fusion | Human fibronectin |
| Chimeric inhibitor | Human fibronectin |
| Protein used in database | Human fibronectin |
| Fibronectin receptor | Human fibronectin |
| Metastasis inhibitor | Human fibronectin |

Method for increasing efficacy of gene transfer to target cell using retrovirus - by infection of the target cell in the presence of a substance which binds to the virus and a substance which binds to the target cell

Claim 42; Pages 97-99; 194pp; Japanese.

The present sequence is a human fibronectin fragment containing a CS-1-binding domain, which was used in the development of a novel method for increasing the efficiency of gene introduction into a target cell using a retroviral vector. The method comprises carrying out viral infection of the target cell in the presence of a retrovirus and target cell binding substance or substances. The method can be used to effectively introduce genes into target cells for the gene therapy of cancer and viral diseases, e.g. AIDS.

Sequence 457 AA:

Query Match 100.0%; Score 2398; DB 18; Length 457;
Best Local Similarity 100.0%; Pred. No. 6e-172;
Matches 457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 PDLRFTNIGPDMRVMTAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
DB 1 PDLRFTNIGPDMRVMTAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
OY 61 PTEEVVSVSSVYEQHESTPLRGKGTGLDPTGIDSDITANSFTVHWIARATITGYR 120
DB 61 PTEEVVSVSSVYEQHESTPLRGKGTGLDPTGIDSDITANSFTVHWIARATITGYR 120
OY 121 IRHHEHESGRRERDVPHSRNSITLTNLTPTGEVVSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHESGRRERDVPHSRNSITLTNLTPTGEVVSIVALNGREESPLLIGQOSTVSD 180
OY 181 VRDLEVVAAATPTSLISMDAPAVRYRYRITYGETGNSPVQEFVTPGSKSTATISGLK 240
DB 181 VRDLEVVAAATPTSLISMDAPAVRYRYRITYGETGNSPVQEFVTPGSKSTATISGLK 240
OY 241 PGVDYTTIYAAVAGKDSPPASSKPTISINRTETIDKPSMAAGSITTLPALPEGGGGAFFP 300
DB 241 PGVDYTTIYAAVAGKDSPPASSKPTISINRTETIDKPSMAAGSITTLPALPEGGGGAFFP 300
OY 301 GHFKDPKRLCKNGGFFFLIHPDGRVDGYREKSDPHIKIQLOAEERGVVSIGVCANRRL 360
DB 301 GHFKDPKRLCKNGGFFFLIHPDGRVDGYREKSDPHIKIQLOAEERGVVSIGVCANRRL 360
OY 361 AMKEDGRLASKCVNDECEFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGQ 420
DB 361 AMKEDGRLASKCVNDECEFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGQ 420
OY 421 KALFLPMSAASDELPLYTLPHPLHGPILLDPST 457
DB 421 KALFLPMSAASDELPLYTLPHPLHGPILLDPST 457

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RESULT 2

ID AAR40160 standard; peptide; 432 AA.

AC AAR40160;

DT 07-FEB-1994 (first entry)

DE Human FN/DFGF fusion peptide #1.

KW Human; fibronectin; FN; fibroblast cell growth factor; FGF;

KW fusion; cell adhesion; cell growth; anti-aging; cosmetics;

OS wound healing; surgery.

XX Homo sapiens.

XX Key

Location/Qualifiers

1..277

Peptide

FT Peptide /note="Human FN fragment 1239-1515"
FT 278..432
FT /note="DFGF fragment"

PN JP05178897-A.

XX 20-JUL-1993.

XX 05-MAR-1992: 92JP-0083220.

XX 14-OCT-1991: 91JP-0291959.

XX (TAKI) TAKARA SHUZO CO LTD.

XX WPI, 1993-261656/33.

DR

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Sequence 432 AA:

Query Match 94.1%; Score 2257; DB 14; Length 432;
Best Local Similarity 99.8%; Pred. No. 2.2e-161;
Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 PDLRFTNIGPDMRVMTAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
DB 1 PDLRFTNIGPDMRVMTAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVYLTNLL 60
OY 61 PTEEVVSVSSVYEQHESTPLRGKGTGLDPTGIDSDITANSFTVHWIARATITGYR 120
DB 61 PTEEVVSVSSVYEQHESTPLRGKGTGLDPTGIDSDITANSFTVHWIARATITGYR 120
OY 121 IRHHEHESGRRERDVPHSRNSITLTNLTPTGEVVSIVALNGREESPLLIGQOSTVSD 180
DB 121 IRHHEHESGRRERDVPHSRNSITLTNLTPTGEVVSIVALNGREESPLLIGQOSTVSD 180
OY 181 VRDLEVVAAATPTSLISMDAPAVRYRYRITYGETGNSPVQEFVTPGSKSTATISGLK 240
DB 181 VRDLEVVAAATPTSLISMDAPAVRYRYRITYGETGNSPVQEFVTPGSKSTATISGLK 240
OY 241 PGVDYTTIYAAVAGKDSPPASSKPTISINRTETIDKPSMAAGSITTLPALPEGGGGAFFP 300
DB 241 PGVDYTTIYAAVAGKDSPPASSKPTISINRTETIDKPSMAAGSITTLPALPEGGGGAFFP 300
OY 301 GHFKDPKRLCKNGGFFFLIHPDGRVDGYREKSDPHIKIQLOAEERGVVSIGVCANRRL 360
DB 301 GHFKDPKRLCKNGGFFFLIHPDGRVDGYREKSDPHIKIQLOAEERGVVSIGVCANRRL 360
OY 361 AMKEDGRLASKCVNDECEFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGQ 420
DB 361 AMKEDGRLASKCVNDECEFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSTGPGQ 420
OY 421 KALFLPMSAAS 432
DB 421 KALFLPMSAAS 432

```

Human FN/DFGF fusion peptide #1.

Human; fibronectin; FN; fibroblast cell growth factor; FGF;

fusion; cell adhesion; cell growth; anti-aging; cosmetics;

wound healing; surgery.

Homo sapiens.

Key

Location/Qualifiers

1..277

Peptide

DT 23-FEB-1998 (first entry)
 XX Human fibroblast growth factor oligopeptide.
 DE
 XX Human; fibroblast growth factor; FGF; target cell;
 KW transfection; retroviral vector; gene therapy; cancer;
 KW viral disease; acquired immunodeficiency syndrome; AIDS.
 XX
 OS Homo sapiens.
 XX
 PM W09718318-A1.
 XX
 XX 22-MAY-1997.
 PD
 XX 07-NOV-1996; 96WO-JP03254.
 PE
 XX 08-MAR-1996; 96JP-0051847.
 PR 13-NOV-1995; 95JP-0294382.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Asada K, Hashino K, Kato I, Koyama N, Uemori T;
 PI Ueno T;
 DR WPI; 1997-289294/26.
 XX
 XX Method for increasing efficacy of gene transfer to target cell using
 PT retrovirus - by infection of the target cell in the presence of a
 PT substance which binds to the virus and a substance which binds to
 PT the target cell
 XX
 PS Claim 42; Pages 94-97; 194pp; Japanese.
 XX
 CC The present sequence is a human fibroblast growth factor (FGF)
 CC oligopeptide, which was used in the development of a novel method
 CC for increasing the efficiency of gene introduction into a target
 CC cell using a retroviral vector. The method comprises carrying out
 CC viral infection of the target cell in the presence of a retrovirus
 CC and target cell binding substance or substances. The method can be
 CC used to effectively introduce genes into target cells for the gene
 CC therapy of cancer and viral diseases, e.g. AIDS.
 CC
 XX
 SQ Sequence 432 AA;
 Query Match 94.1%; Score 2257; DB 18; Length 432;
 Best Local Similarity 99.8%; Pred. No. 2.2e-161;
 Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Y 1 PTDLRFNTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEDVAELISPSDNAVLTNLL 60
 DB 1 PTDLRFNTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEDVAELISPSDNAVLTNLL 60
 QY 61 PGTETVYVSVSYEHESTPLRGROKTGLDPTGIDFSDITANSFYVHWIAPRATITGYR 120
 DB 61 PGTETVYVSVSYEHESTPLRGROKTGLDPTGIDFSDITANSFYVHWIAPRATITGYR 120
 QY 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 DB 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 QY 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 DB 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 QY 181 VRDLEEVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQEFVPGSKSTATISGLK 240
 DB 181 VRDLEEVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQEFVPGSKSTATISGLK 240
 QY 241 PGVDYITTYAVTGRDPSASSKPISINYTEIDKPSMAAGSTITLPALEDDGSGAFPP 300
 DB 241 PGVDYITTYAVTGRDPSASSKPISINYTEIDKPSMAAGSTITLPALEDDGSGAFPP 300
 QY 301 GHFKDKPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKIQLOAEERGVSISIKVCANRYL 360
 DB 301 GHFKDKPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKIQLOAEERGVSISIKVCANRYL 360
 QY 361 AMKEDGRLASKCVTDECFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPQ 420

DB 361 AMKEDGRLASKCVTDECFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPQ 420
 QY 421 KALFLPMSAAS 432
 DB 421 KALFLPMSAKS 432
 RESULT 4
 AA05457
 ID AAY05457 standard; protein; 432 AA.
 XX
 XX AAY05457;
 AC
 XX 07-JUL-1999 (first entry)
 DT
 XX Fibronectin receptor targeting HIV strain C-FGF.A.
 DE Fibronectin receptor; HIV; infection; therapy.
 KW Fibronectin receptor; HIV; infection; therapy.
 XX
 OS Unidentified.
 XX
 PM JP10029952-A.
 PN
 XX 03-FEB-1998.
 PD
 XX 16-JUL-1996; 96JP-0185893.
 PR 16-JUL-1996; 96JP-0185893.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI WPI; 1998-163674/15.
 DR
 XX Control of human immunodeficiency virus infection - using
 PT composition comprising replication defective HIV vector
 PT
 XX
 PS Example 3; Page 21-22; 24pp; Japanese.
 XX
 CC This sequence represents a fibronectin receptor that can be used in
 CC the method of the invention. The method is for the control of human
 CC immunodeficiency virus (HIV) infection using a composition which
 CC comprises a functional substance which participates in the infection of
 CC HIV. The method is used to control HIV-infection.
 CC
 XX
 SQ Sequence 432 AA;
 Query Match 94.1%; Score 2257; DB 19; Length 432;
 Best Local Similarity 99.8%; Pred. No. 2.2e-161;
 Matches 431; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PTDLRFNTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEDVAELISPSDNAVLTNLL 60
 DB 1 PTDLRFNTNIGPDTMRYTAPPSIDLTNPLVRYSPVKNEDVAELISPSDNAVLTNLL 60
 QY 61 PGTETVYVSVSYEHESTPLRGROKTGLDPTGIDFSDITANSFYVHWIAPRATITGYR 120
 DB 61 PGTETVYVSVSYEHESTPLRGROKTGLDPTGIDFSDITANSFYVHWIAPRATITGYR 120
 QY 61 PGTETVYVSVSYEHESTPLRGROKTGLDPTGIDFSDITANSFYVHWIAPRATITGYR 120
 DB 61 PGTETVYVSVSYEHESTPLRGROKTGLDPTGIDFSDITANSFYVHWIAPRATITGYR 120
 QY 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 DB 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 QY 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 DB 121 IRHHPEHFSGRPREDRVPHSRNSITLTNLTPTGETVYVSIALNGREESPLLIGQOSTVSD 180
 QY 181 VRDLEEVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQEFVPGSKSTATISGLK 240
 DB 181 VRDLEEVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQEFVPGSKSTATISGLK 240
 QY 241 PGVDYITTYAVTGRDPSASSKPISINYTEIDKPSMAAGSTITLPALEDDGSGAFPP 300
 DB 241 PGVDYITTYAVTGRDPSASSKPISINYTEIDKPSMAAGSTITLPALEDDGSGAFPP 300
 QY 301 GHFKDKPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKIQLOAEERGVSISIKVCANRYL 360
 DB 301 GHFKDKPKRLCYCKNGGFFLRIHPDGRVDGVRKESDPHIKIQLOAEERGVSISIKVCANRYL 360

CC be useful in prevention of metastasis and tumour growth, as a con-
 CC traceptive, for the treatment of e.g. osteoporosis, retinopathy and
 CC rheumatism and to inhibit the spread of foci in psoriasis.

XX Sequence 574 AA:

Query Match 64.1%; Score 1536.5; DB 11; Length 574;
 Best Local Similarity 58.0%; Pred. No. 4.3e-107;
 Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PDLRLTNGPDMRYMAYAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60
 DB 1 PDLRLTNGPDMRYMAYAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60
 QY 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYHMTAPRATTIGYR 120
 DB 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYHMTAPRATTIGYR 120
 QY 121 IRHHEHFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGREESPLLIGQSTVSD 180
 DB 121 IRHHEHFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGREESPLLIGQSTVSD 180
 QY 181 VRDLEVAATPTSLISMDAPAVYRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
 DB 181 VRDLEVAATPTSLISMDAPAVYRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
 QY 241 PGVDYITTYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297
 DB 241 PGVDYITTYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297
 QY 298 FPPGHEKDKPRLYCKNGGFELRHDPGRVDGYREKSDPHIKILOAEERGVSIGVCAN 357
 DB 298 FPPGHEKDKPRLYCKNGGFELRHDPGRVDGYREKSDPHIKILOAEERGVSIGVCAN 357
 QY 301 TPEN-----VQLTGVRVATP-----KEKTPMKKEINLADSSVYVGLMVAAT 344
 DB 301 TPEN-----VQLTGVRVATP-----KEKTPMKKEINLADSSVYVGLMVAAT 344
 QY 358 RY-----LAMKEDGRLLASK-----CYTDEC----- 378
 DB 358 RY-----LAMKEDGRLLASK-----CYTDEC----- 378
 QY 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401
 DB 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401
 QY 379 FFERLESNNYNTYRS-----RKYT----- 398
 DB 379 FFERLESNNYNTYRS-----RKYT----- 398
 QY 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKIYLYTLNDNARSSPVVIDASTAI 461
 DB 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKIYLYTLNDNARSSPVVIDASTAI 461
 QY 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417
 DB 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417
 QY 462 DAPSNLRFATTPNSLSLWMPPRARITGYIIEKPGSPPREVVRPRRGVTEATITGL 521
 DB 462 DAPSNLRFATTPNSLSLWMPPRARITGYIIEKPGSPPREVVRPRRGVTEATITGL 521
 QY 418 -PGOKAILFL-----PM--SAASDELPLQVTLPHPNLHGPEILDVPST 457
 DB 418 -PGOKAILFL-----PM--SAASDELPLQVTLPHPNLHGPEILDVPST 457
 b 522 EPGETEYTIYVIALKNQKSEPLIGRKKTDELPLQVTLPHPNLHGPEILDVPST 574

RESULT 7

AAW60351 standard; protein; 574 AA.

AC AAW60351;

XX 01-MAR-1995 (first entry)

XX Inhibitory Fibronectin receptor affinity protein.

XX fibronectin receptor; cell adhesion activity region; abnormal cells;

XX inhibitor; affinity; treatment; diagnostic agent; AIDS; cancer;

XX autoimmune deficiency syndrome; heparin binding.

OS Chimeric Homo sapiens.

XX Key Location/Qualifiers

XX Domain 255..258

XX /label= RGDS_motif

XX JP06172203-A.

PD 21-JUN-1994.

XX 02-DEC-1992; 92JP-0345170.

XX 02-DEC-1992; 92JP-0345170.

XX (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1994-238664/29.

XX Fibronectin receptor-producing an abnormal cell inhibitor -

XX useful in treatment and diagnosis of AIDS and cancer

XX Claim 1; Page 22-23; 24pp; Japanese.

CC The inhibitory polypeptide has an affinity for the FR (and is used
 CC to derive other chimeric polypeptides: AAW60348-54), and is based on
 CC the cell adhesion activity region of human fibronectin. All the
 CC peptides of the invention contain an RGDS motif. The inhibitor
 CC can be used as a therapeutic and diagnostic agent for AIDS and
 CC cancers. (See also AAW60343-47).

XX Sequence 574 AA:

Query Match 64.1%; Score 1536.5; DB 15; Length 574;
 Best Local Similarity 58.0%; Pred. No. 4.3e-107;
 Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PDLRLTNGPDMRYMAYAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60
 DB 1 PDLRLTNGPDMRYMAYAPPSIDLTNLFVRSYKNEEDVAELISPSDNAVLTNLL 60

QY 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYHMTAPRATTIGYR 120
 DB 61 PGEYVSVSSVYEOHESFPLRGOKTGIDSPGIDFSITANSFYHMTAPRATTIGYR 120

QY 121 IRHHEHFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGREESPLLIGQSTVSD 180
 DB 121 IRHHEHFGSRPREDRVPHSRNSITLNLPGTEYVSVIALNGREESPLLIGQSTVSD 180

QY 181 VRDLEVAATPTSLISMDAPAVYRYRITYGETGNSPVQEFVPGSKSTATISGLK 240
 DB 181 VRDLEVAATPTSLISMDAPAVYRYRITYGETGNSPVQEFVPGSKSTATISGLK 240

QY 241 PGVDYITTYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297
 DB 241 PGVDYITTYAVTGRDSPAASKPISINRTEIDKPSMAGSTTL--PALPEDGSGA 297

QY 298 FPPGHEKDKPRLYCKNGGFELRHDPGRVDGYREKSDPHIKILOAEERGVSIGVCAN 357
 DB 298 FPPGHEKDKPRLYCKNGGFELRHDPGRVDGYREKSDPHIKILOAEERGVSIGVCAN 357

QY 301 TPEN-----VQLTGVRVATP-----KEKTPMKKEINLADSSVYVGLMVAAT 344
 DB 301 TPEN-----VQLTGVRVATP-----KEKTPMKKEINLADSSVYVGLMVAAT 344

QY 358 RY-----LAMKEDGRLLASK-----CYTDEC----- 378
 DB 358 RY-----LAMKEDGRLLASK-----CYTDEC----- 378

QY 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401
 DB 345 KYEVSVYALKD---TLTSRPAQGVVTTLENVSPRRARVDAETTTISWRTKETITG 401

QY 379 FFERLESNNYNTYRS-----RKYT----- 398
 DB 379 FFERLESNNYNTYRS-----RKYT----- 398

QY 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKIYLYTLNDNARSSPVVIDASTAI 461
 DB 402 FOYDAVPANGQPIQRTITPDVRSYTTTGLQPTDYKIYLYTLNDNARSSPVVIDASTAI 461

QY 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417
 DB 399 -----SMYVALKRTGOY-----KLGSK-----TG- 417

QY 462 DAPSNLRFATTPNSLSLWMPPRARITGYIIEKPGSPPREVVRPRRGVTEATITGL 521
 DB 462 DAPSNLRFATTPNSLSLWMPPRARITGYIIEKPGSPPREVVRPRRGVTEATITGL 521

QY 418 -PGOKAILFL-----PM--SAASDELPLQVTLPHPNLHGPEILDVPST 457
 DB 418 -PGOKAILFL-----PM--SAASDELPLQVTLPHPNLHGPEILDVPST 457

XX 522 EPGETEYTIYVIALKNQKSEPLIGRKKTDELPLQVTLPHPNLHGPEILDVPST 574

RESULT 8

AAW33349 standard; protein; 574 AA.

XX AAW33349

| CC | HIV. The method is used to control HIV-infection. | |
|----|--|--|
| XX | Sequence 574 AA: | |
| XX | Query Match 64.1%; score 1536.5; DB 19; Length 574; | |
| XX | Best Local Similarity 58.0%; Pred. No. 4.3e-107; | |
| XX | Matches 344; Conservative 26; Mismatches 66; Indels 155; Gaps 14; | |
| CC | | |
| XX | 1 PNDLFTNIGPDMRTMTAPPSIDLTNLFVRYSPVKNEEDVAELISPSDNAVLTNLL 60 | |
| XX | 1 PDLFTNIGPDMRTMTAPPSIDLTNLFVRYSPVKNEEDVAELISPSDNAVLTNLL 60 | |
| XX | 61 PCTEVVSVSSVYEEHESPTLRGROKGTGLDSEPTGIDFSDITANSTVHMIAPRATITGYR 120 | |
| XX | 61 PCTEVVSVSSVYEEHESPTLRGROKGTGLDSEPTGIDFSDITANSTVHMIAPRATITGYR 120 | |
| XX | 121 INHHEHESGPREDRVPRSRNSITLNTLPCTEVVSVSVALNGEESPLLIGQOSTSD 180 | |
| XX | 121 INHHEHESGPREDRVPRSRNSITLNTLPCTEVVSVSVALNGEESPLLIGQOSTSD 180 | |
| XX | 181 VRDLEVVAAATPTSLISMDAPAVTVRRYRIYGETGNSPPOEFTVGSKSTATISGLK 240 | |
| XX | 181 VRDLEVVAAATPTSLISMDAPAVTVRRYRIYGETGNSPPOEFTVGSKSTATISGLK 240 | |
| XX | 241 PGVDYTTIVYAVTAGRGDSPAASKPISINRYEIDKPSMAAGSITTL--PALPEDGSGCA 297 | |
| XX | 241 PGVDYTTIVYAVTAGRGDSPAASKPISINRYEIDKPSMAIPAPDLKFTQVPTSLSAQW 300 | |
| XX | 298 PFPGFHKDPKRLCYKNGGFELRIHDDGKVDGVRKESDPRIKQLQDAERGVSISGVCAN 357 | |
| XX | 301 TPEPN-----VLTGTVRYRVT-----KEKTGPKKEINLAPDSSSVVSGLMVAT 344 | |
| XX | 358 RY-----LAWKEDGRLLASK-----CVTDEC----- 378 | |
| XX | 345 KVEVSYALKD--ILTSRPAQGVYTTLENVSPPRARVTDATETTTIISMTKTEITTG 401 | |
| XX | 379 FEEFERLESNNYNTYRS-----RKYT----- 398 | |
| XX | 402 PQVDVAVPANGQTPIDRTIKPDVRSYTTIGLQGTQDYKIYLTLANMARSPVYIDASTAI 461 | |
| XX | 399 -----SMYALKRTGOY-----KLQSK-----TG- 417 | |
| XX | 462 DAPSNLRLATTPNLSILVSMQPPRARITGYIILKYEKPGSPPREVVPRRPGVTEATITGL 521 | |
| XX | 418 -GGQAKAIIEL-----PW--SAASDELPOLVTLRPHNLHGPEIILDVST 457 | |
| XX | 522 EPGTEYTTIVYALKNNQKSEPLIGRKKTDLPOLVTLRPHNLHGPEIILDVST 574 | |
| XX | RESULT 11 | |
| XX | AAM97357 | |
| XX | ID AAM97357 standard; peptide: 574 AA. | |
| XX | XX AAM97357: | |
| XX | DT 12-MAY-1999 (first entry) | |
| XX | DE Protein sequence of the specification. | |
| XX | KW Retrovirus; gene transfer; serum-free medium; AIDS; cancer; | |
| XX | KM leukaemia; gene therapy. | |
| XX | OS Homo sapiens. | |
| XX | PN W09905301-A1. | |
| XX | PD 04-FEB-1999. | |
| XX | PF 15-JUL-1998; 98WO-JP03173. | |
| XX | PR 23-JUL-1997; 97JP-0196772. | |
| XX | PA (TAKI) TAKARA SHUZO CO LTD. | |

XX Baguis C, Imbert A, Mannoni P;
 XX WPI: 1999-142951/12.
 DR Gene transfer by retrovirus in medium containing functional
 XX substance and optionally low-density lipoprotein - useful in medical
 PT sciences, cell and gene engineering, particularly for treating AIDS
 PT and cancers
 XX
 PS Claim 5; Page 27-30; 32pp; Japanese.
 XX
 CC The specification describes a method for transferring a gene into
 CC target cells by a retrovirus using a serum-free medium. The culture
 CC medium of the target cells is serum free and contains an effective
 CC amount of a functional substance to elevate the gene transfer efficiency
 CC when both the retrovirus and target cells are present together. The
 CC gene transfer method is useful in medical sciences, cell engineering
 CC and genetic engineering, such as in the treatment of AIDS and cancers
 e.g. leukaemia by gene therapy.

Sequence 574 AA:

Query Match 64.1%; Score 1536.5; DB 20; Length 574;
 Best Local Similarity 58.0%; Pred. No. 4.3e-107;
 Matches 344; Conservative 26; Mismatches 68; Indels 155; Gaps 14;

QY 1 PTDLFTNIGPPTMRTVMAAPPSPIDLTNPLVRSYVKNEEDVAELTSPSDMAVYLTNLL 60
 DB 1 PTDLFTNIGPPTMRTVMAAPPSPIDLTNPLVRSYVKNEEDVAELTSPSDMAVYLTNLL 60
 QY 61 PCTEVVSVSSYVEQHESTPLRGROKGTGDSPTGIDFSDTANSTVMIAPRATITGCR 120
 DB 61 PCTEVVSVSSYVEQHESTPLRGROKGTGDSPTGIDFSDTANSTVMIAPRATITGCR 120
 QY 121 IRHHPHESGRRPREDRVPHSRNSITLNLPTGETEVVSIVALNGREESPLLIGQOSTVSD 180
 DB 121 IRHHPHESGRRPREDRVPHSRNSITLNLPTGETEVVSIVALNGREESPLLIGQOSTVSD 180
 QY 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240
 DB 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240
 QY 241 PGVDYTIIVYAVTGRGDSBASSKPTISINVRTEIDRPSMAAGSITL---PALPEDGSGGA 297
 DB 241 PGVDYTIIVYAVTGRGDSBASSKPTISINVRTEIDRPSMAAGSITL---PALPEDGSGGA 297
 QY 298 FPPGHFKDPRKRLYCKNGCFELRIHDPGRVDGVRKSDPIKIQLOAEERGVSISIGVCAN 357
 DB 298 FPPGHFKDPRKRLYCKNGCFELRIHDPGRVDGVRKSDPIKIQLOAEERGVSISIGVCAN 357
 QY 301 TTPPN-----VQLTGVRVPT-----KEKTGPKKEINLAPDSSVVVSGIMVAT 344
 DB 301 TTPPN-----VQLTGVRVPT-----KEKTGPKKEINLAPDSSVVVSGIMVAT 344
 QY 358 RY-----LAMKEDGRLASK-----CVTDEC----- 378
 DB 358 RY-----LAMKEDGRLASK-----CVTDEC----- 378
 QY 345 KYEVSVALKMD---TLTSRPAQGVTTLENSPPRARAVTDTETITISMTKRETTIG 401
 DB 345 KYEVSVALKMD---TLTSRPAQGVTTLENSPPRARAVTDTETITISMTKRETTIG 401
 QY 379 FEEFELSENNNNTYS-----RKYT----- 398
 DB 379 FEEFELSENNNNTYS-----RKYT----- 398
 QY 402 FOVDVVPANGOTPIORTIKPDKVRSITITIGLPGCTDYKIITLYLNDNANSSPVVIDASTAI 461
 DB 402 FOVDVVPANGOTPIORTIKPDKVRSITITIGLPGCTDYKIITLYLNDNANSSPVVIDASTAI 461
 QY 399 -----SWYVALKRTGOY-----KLGSK-----TG- 417
 DB 399 -----SWYVALKRTGOY-----KLGSK-----TG- 417
 QY 462 DAPSNLRELATTPNSLLVSMOPPRARITGIYIKERKPSGPREVVRPRPGVTEATTIGL 521
 DB 462 DAPSNLRELATTPNSLLVSMOPPRARITGIYIKERKPSGPREVVRPRPGVTEATTIGL 521
 QY 418 -PGOKAIFL-----PW-SASADELPOLVTLPHPNLHGEILDVPS 457
 DB 418 -PGOKAIFL-----PW-SASADELPOLVTLPHPNLHGEILDVPS 457
 QY 522 EBGTEYTIIVIALKNKOKSEPLIGRKKTDDELPLQVTLPHPNLHGEILDVPS 574
 DB 522 EBGTEYTIIVIALKNKOKSEPLIGRKKTDDELPLQVTLPHPNLHGEILDVPS 574

RESULT 12
 AAM33343
 ID AAM33343 standard; protein; 489 AA.
 XX
 AC AAM33343;

XX 23-FEB-1998 (first entry)
 DT Protein used in development of gene transfer method.
 XX
 DE Target cell; transfection; retroviral vector; gene therapy; cancer;
 XX viral disease; acquired immunodeficiency syndrome; AIDS.
 KW Synthetic.
 XX
 OS
 XX
 PM WO9718318-A1.
 PD 22-MAY-1997.
 XX
 PD 07-NOV-1996; 96WO-JP03254.
 PF
 XX 08-MAR-1996; 96JP-0051847.
 PR 13-NOV-1995; 95JP-0294382.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 XX Asada K, Hashino K, Kato I, Koyama N, Uemori T;
 PI Ueno T;
 PI
 DR WPI: 1997-289294/26.
 XX
 PT Method for increasing efficacy of gene transfer to target cell using
 PT retrovirus - by infection of the target cell in the presence of a
 PT substance which binds to the virus and a substance which binds to
 PT the target cell

XX
 PS Claim 45; Pages 104-107; 194pp; Japanese.
 XX
 CC The present sequence was used in the development of a novel method
 CC for increasing the efficiency of gene introduction into a target
 CC cell using a retroviral vector. The method comprises carrying out
 CC viral infection of the target cell in the presence of a retrovirus
 CC and target cell binding substance or substances. The method can be
 CC used to effectively introduce genes into target cells for the gene
 CC therapy of cancer and viral diseases, e.g. AIDS.
 CC
 SO Sequence 489 AA;

Query Match 63.7%; Score 1527; DB 18; Length 489;
 Best Local Similarity 65.5%; Pred. No. 1.8e-106;
 Matches 342; Conservative 7; Mismatches 75; Indels 98; Gaps 11;

QY 1 PTDLFTNIGPPTMRTVMAAPPSPIDLTNPLVRSYVKNEEDVAELTSPSDMAVYLTNLL 60
 DB 1 PTDLFTNIGPPTMRTVMAAPPSPIDLTNPLVRSYVKNEEDVAELTSPSDMAVYLTNLL 60
 QY 61 PCTEVVSVSSYVEQHESTPLRGROKGTGDSPTGIDFSDTANSTVMIAPRATITGCR 120
 DB 61 PCTEVVSVSSYVEQHESTPLRGROKGTGDSPTGIDFSDTANSTVMIAPRATITGCR 120
 QY 121 IRHHPHESGRRPREDRVPHSRNSITLNLPTGETEVVSIVALNGREESPLLIGQOSTVSD 180
 DB 121 IRHHPHESGRRPREDRVPHSRNSITLNLPTGETEVVSIVALNGREESPLLIGQOSTVSD 180
 QY 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240
 DB 181 VPRDLEVAAPPTSLISMDAPAVTVRRYRITYGETGNSPVQEFPTVPGSKSTATISGLK 240
 QY 241 PGVDYTIIVYAVTGRGDSBASSKPTISINVRTEIDRPSMAAGSITL---PALPEDGSGG- 296
 DB 241 PGVDYTIIVYAVTGRGDSBASSKPTISINVRTEIDRPSMAAGSITL---PALPEDGSGG- 296
 QY 297 -----APPGHF-----KDKPRLYCKNG-----GFFLRTH 321
 DB 297 -----APPGHF-----KDKPRLYCKNG-----GFFLRTH 321
 QY 301 DMGIRGDRGEIGPGRGDPGEPKGRGPGDGLGPPGPKGLGVPGLPGVPGRG 360
 DB 301 DMGIRGDRGEIGPGRGDPGEPKGRGPGDGLGPPGPKGLGVPGLPGVPGRG 360
 QY 322 PDGRVD-----GVREKSDPIKIQLOAEERGVSISIGVCANRYLAKKE--- 364
 DB 322 PDGRVD-----GVREKSDPIKIQLOAEERGVSISIGVCANRYLAKKE--- 364

Db 361 PKSGIGPGPGANGKGGKGTGPKGPPR-----GGRGPTGPRGGERGPRGIGTGKPKGK 413
 QY 365 -----DGRLLASKCVYDECFEERLESNNYNTYRSKRYTSWYALKRTGQYKLGSTGPG 419
 Db 414 GNSGDDGPPAGPPG-----ERGFNGPQGP-----TG--FPGPKGPPG 447
 QY 420 OKAILFLP-----MSASDELPLQVTLPHPHNLHGPELIDVPST 457
 Db 448 PPGKDGLPGRHPPGGRASDELPLQVTLPHPHNLHGPELIDVPST 489
 RESULT 13
 AAR60350
 ID AAR60350 standard; protein; 573 AA.
 XX AAR60350;
 AC AAR60350;
 DT 01-MAR-1995 (first entry)
 XX
 XX Chimeric Inhibitory Fibronectin receptor affinity protein 3.
 DE
 KW fibronectin receptor; cell adhesion activity region; abnormal cells;
 KW inhibitor; affinity; treatment; diagnostic agent; AIDS; cancer;
 KW autoimmunity deficiency syndrome; heparin binding.
 XX
 XX Chimeric Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Domain 255..258
 FT /label= RGDs_motif
 PN JP06172203-A.
 XX 21-JUN-1994.
 XX
 XX 02-DEC-1992; 92JP-0345170.
 XX
 XX 02-DEC-1992; 92JP-0345170.
 XX
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 DR WPI; 1994-238664/29.
 XX
 PT Fibronectin receptor-producing an abnormal cell inhibitor -
 PT useful in treatment and diagnosis of AIDS and cancer
 XX
 PS Claim 1; Page 15-16; 24pp; Japanese.
 XX
 CC AAR60348-55 are chimeric human protein inhibitors of abnormal cells
 CC which produce fibronectin receptors (FR). These inhibitory
 CC polypeptides have an affinity for the FRs (and are based on AAR60356),
 CC and are based on the cell adhesion activity region of human
 CC fibronectin. AAR60348-53 are multifunctional and can also bind heparin.
 CC The inhibitor can be used as a therapeutic and diagnostic agent for
 CC AIDS and cancers. (See also AAR60343-47).
 CC
 XX
 XX
 SQ Sequence 573 AA:
 Query Match 63.5%; Score 1523; DB 15; Length 573;
 Best Local Similarity 57.6%; Pred. No. 4,5e-106;
 Matches 341; Conservative 26; Mismatches 71; Indels 154; Gaps 14;
 QY 1 PDDLRTNIGPDMRTYMAPPSIDLTNPLVRSYKNEEDVAELISPSDNAVLTNLL 60
 Db 1 PDDLRTNIGPDMRTYMAPPSIDLTNPLVRSYKNEEDVAELISPSDNAVLTNLL 60
 QY 61 PGTVEVVSYSVEQHESTPLRGKRTGLDPTGIDFSDITANSFTVHMATPATITGYR 120
 Db 61 PGTVEVVSYSVEQHESTPLRGKRTGLDPTGIDFSDITANSFTVHMATPATITGYR 120
 QY 121 IRHHPEHFGRPREDRVPHSRNSITLTNLTPTGEVVSIVALNGREESPLLIGQSTVSD 180
 Db 121 IRHHPEHFGRPREDRVPHSRNSITLTNLTPTGEVVSIVALNGREESPLLIGQSTVSD 180

QY 181 VPREDLEVATPTSLISMDAPAVTVRYRITYGENTGNSPVOEFTVPGSKSTATISGLK 240
 Db 181 VPREDLEVATPTSLISMDAPAVTVRYRITYGETGNSPVOEFTVPGSKSTATISGLK 240
 QY 241 PGVDYITTYAAVAGRDSPASSKPSISINVTEDIDKPSM--AAGSITTLPALPEDGGSGAF 298
 Db 241 PGVDYITTYAAVAGRDSPASSKPSISINVTEDIDKPSAIPAPTDLKFTQVTPTSLSAQMT 300
 QY 299 PPGHEKDPKRLKNGGFFELRIHPDGRVDGVRKSDPHIKLQLOAERGVSISIKVCANR 358
 Db 301 PPN-----VQLTGVRVRYTP-----KEKTPMKKEINLAPDSSVVSGLMWATK 344
 QY 359 Y-----LAMEKDGRLASK-----CYVDEC-----F 379
 Db 345 YEVSYYALKD---TLTSRPAQGVVTLLENVSPRRARVDATETTTISWRTETITG 401
 QY 380 FFERLESNNYNTYRS--RKYT-----TG-- 417
 Db 402 QVDAVAVANQGTPTQRTIKPDVRSYTTTGLQPGTDYKIYLTLDNARSSPVYIDASTAID 461
 QY 399 -----SWYVALKRTGQY-----KLGSK----- 417
 Db 462 APSNLFRLATTPNSLIVSQPPRARITGYTIKYEKSPPREVPPRPGVTEATITGLE 521
 QY 418 PGOKAILFLP-----PM--SAASDELPLQVTLPHPHNLHGPELIDVPST 457
 Db 522 PGTETTYVIALKKNKSEPLIGRKKTDELPLQVTLPHPHNLHGPELIDVPST 573
 RESULT 14
 AAM38647
 ID AAM38647 standard; protein; 2265 AA.
 XX AAM38647;
 AC AAM38647;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 DE Human polypeptide SEQ ID NO 1792.
 XX
 XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 XX Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34263.
 XX
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 XX (HYTE-) HYSBO INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 XX WPI: 2001-442253/47.
 DR N-PDB: AA157803.
 XX

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

Example 3: SEQ ID NO 1792; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA157798-AA161369) with neurotrophic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Other uses include the utilisation of the activities such as: immune system suppression, cell activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

Sequence 2265 AA;

Query Match 62.6%; Score 1501; DB 22; Length 2265;
Best Local Similarity 49.8%; Pred. No. 1.2e-103;
Matches 341; Conservative 33; Mismatches 55; Indels 256; Gaps 14;

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1  PTDLFTNTGPTMTVMAAPPSPIDLTNLFVRSVPKNEDEVAELISPSDNAVYLTNLL 60
Db 1270 PTDLFTNTGPTMTVMAAPPSPIDLTNLFVRSVPKNEDEVAELISPSDNAVYLTNLL 1329
OY 1  PTDLFTNTGPTMTVMAAPPSPIDLTNLFVRSVPKNEDEVAELISPSDNAVYLTNLL 60
OY 61  PGTETVVSVSSVYEQHESPLRGKRGKTGLDPTGIDFSDITANSFTVMHIAARATTGGR 120
Db 1330 PGTETVVSVSSVYEQHESPLRGKRGKTGLDPTGIDFSDITANSFTVMHIAARATTGGR 1389
OY 121 IRHHEHESGRREDRVPHSRNSITLTNLTPTETEVVSIVALNGRESPLLIGQOSTVSD 180
Db 1390 IRHHEHESGRREDRVPHSRNSITLTNLTPTETEVVSIVALNGRESPLLIGQOSTVSD 1449
OY 181 VRDLEVVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQETVPQSKSTATISGLK 240
Db 1450 VRDLEVVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQETVPQSKSTATISGLK 1509
OY 241 PGVDYTIIVYAAVAGRGDSPPASSKPSISINRTEDIKRPSMA-----AGSITTEPA--- 288
Db 1510 PGVDYTIIVYAAVAGRGDSPPASSKPSISINRTEDIKRPSMA-----AGSITTEPA--- 1569
OY 289 -----LPEDGSGAFPPGHEKDKP-----RLYCKN----- 313
Db 1570 TGYRVTTTPKNG-----PGPTKTKTAGPDQTEMTIEGLQPTVEYVSVYAQNPGESQAP 1623
OY 314 -----GGFFLRHHPDGRVDGVRKESDPHT 337
Db 1624 LVQAVATTIPATDLKFTQVPTSLSAQWTPPNVQLTGYRVAVTP-----KKTGPMK 1676
OY 338 KQLOAEEGVVSTIGVCANRY-----LAMKE----- 364
Db 1677 ETLNLPDSSSVVSGLMATKTEVSVYALKDQLTSRPAQGVYTTILENSPPRRARVTDAT 1736
OY 365 -----DGLASKCV-----TDECFEERL 384
Db 1737 ETTTISMTKETETTTGFOVDVAVPANGQPTIORFTIKPDVRSYTTTGLQLOPDTYKITYLVYL 1796
OY 385 ESN-----NYNTRSR----- 395
Db 1797 NDMASSPVVIDASTAIDAPSNMLRLATTPNLSLWSQPPRARITGYITIKYKPPSPPRE 1856
OY 386 -----KTSMYVALKRTGQYKLGSKTGP--GOKAIFLPMASAS 432
Db 1857 VVPRPRPGVTEATIPGLEGTETTYIVIALKN-----NOKSEPLIGRK-----KT 1901
OY 433 DELPOLVTLPHPNLHGPEILDVPS 457

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Db 1902 DELPOLVTLPHPNLHGPEILDVPS 1926

RESULT 15

ID AAR60355 standard; protein; 302 AA.

AC AAR60355;

DT 01-MAR-1995 (first entry)

DE Chimeric inhibitory Fibronectin receptor affinity protein 8.

KM Fibronectin receptor; cell adhesion activity region; abnormal cells;

KW inhibitor; affinity; treatment; diagnostic agent; AIDS; cancer;

KW autoimmunity deficiency syndrome; heparin binding.

OS Chimeric Homo sapiens.

Key Location/Qualifiers

FT Domain 255..258

FT JP06172203-A.

PD 21-JUN-1994.

PF 02-DEC-1992; 92JP-0345170.

PR 02-DEC-1992; 92JP-0345170.

PA (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1994-238664/29.

PT Fibronectin receptor-producing an abnormal cell inhibitor -

PT useful in treatment and diagnosis of AIDS and cancer

PS Claim 1: Page 21-22; 24pp; Japanese.

CC AAR60348-55 are chimeric human protein inhibitors of abnormal cells

CC which produce fibronectin receptors (FR). These inhibitory

CC polypeptides have an affinity for the FRs (and are based on AAR60356),

CC and are based on the cell adhesion activity region of human

CC fibronectin. The inhibitor can be used as a therapeutic and diagnostic

CC agent for AIDS and cancers. (See also AAR60343-47).

Sequence 302 AA;

Query Match 61.9%; Score 1485.5; DB 15; Length 302;
Best Local Similarity 66.1%; Pred. No. 1.3e-103;
Matches 302; Conservative 0; Mismatches 0; Indels 155; Gaps 1;

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1  PTDLFTNTGPTMTVMAAPPSPIDLTNLFVRSVPKNEDEVAELISPSDNAVYLTNLL 60
Db 1 PTDLFTNTGPTMTVMAAPPSPIDLTNLFVRSVPKNEDEVAELISPSDNAVYLTNLL 60
OY 1  PTDLFTNTGPTMTVMAAPPSPIDLTNLFVRSVPKNEDEVAELISPSDNAVYLTNLL 60
OY 61  PGTETVVSVSSVYEQHESPLRGKRGKTGLDPTGIDFSDITANSFTVMHIAARATTGGR 120
Db 61 PGTETVVSVSSVYEQHESPLRGKRGKTGLDPTGIDFSDITANSFTVMHIAARATTGGR 120
OY 121 IRHHEHESGRREDRVPHSRNSITLTNLTPTETEVVSIVALNGRESPLLIGQOSTVSD 180
Db 121 IRHHEHESGRREDRVPHSRNSITLTNLTPTETEVVSIVALNGRESPLLIGQOSTVSD 180
OY 121 IRHHEHESGRREDRVPHSRNSITLTNLTPTETEVVSIVALNGRESPLLIGQOSTVSD 180
Db 121 IRHHEHESGRREDRVPHSRNSITLTNLTPTETEVVSIVALNGRESPLLIGQOSTVSD 180
OY 181 VRDLEVVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQETVPQSKSTATISGLK 240
Db 181 VRDLEVVAAATPTSLISMDAPAVTVRYRYRTYGETGNSPVQETVPQSKSTATISGLK 240
OY 241 PGVDYTIIVYAAVAGRGDSPPASSKPSISINRTEDIKRPSMAAGSITLPALEPDGSGAFPP 300
Db 241 PGVDYTIIVYAAVAGRGDSPPASSKPSISINRTEDIKRPSMAAGSITLPALEPDGSGAFPP 300

```

OY 301 GHFKDPKRLCYCKNGGFELRIHPDGRVDGVREKSDPHIKLQLAERGVVSIGVCANRYL 360
Db 277 ----- 276
OY 361 AMKEDGRLLASKCVYDECFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPGQ 420
Db 277 ----- 276
OY 421 KALFLPMASADELPQVTLPHPNLHGPEILDVPST 457
 |||||
Db 277 -----SDELPQVTLPHPNLHGPEILDVPST 302

Search completed: March 13, 2003, 08:21:14
Job time : 74 secs

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QY 255 RQDSFASPKPISINRYEIDKPSMAAGSITTLPALPEDGSGAFPPGHFKDPKRLCYCKNG 314
 Db 329 --ETVPSQNSHPQIOMLDDDDK---AAGSITTLPALPEDGSGAFPPGHFKDPKRLCYCKNG 383
 QY 315 GFFLRHDPDGVDRGVRKSDPHIKLOLAERGVVSIKVCANRYLAMKEDGRLLASKCV 374
 Db 384 GFFLRHDPDGVDRGVRKSDPHIKLOLAERGVVSIKVCANRYLAMKEDGRLLASKCV 443
 QY 375 TDECFEFLRLESNNYNTYRSRKYTSWYVALKRTGQYKLGSGTGOKAILFLPMSAAS 432
 Db 444 TDECFEFLRLESNNYNTYRSRKYTSWYVALKRTGQYKLGSGTGOKAILFLPMSAAS 501

RESULT 2
 US-09-902-773A-4
 ; Sequence 4, Application US/09902773A
 ; Patent No. US20020034787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HU, JING-SHAN
 ; GOCANE, JEANNINE D.
 ; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-10
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: US
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/09/902,773A
 ; FILING DATE: 12-Jul-2001
 ; CLASSIFICATION: <unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/803,926
 ; FILING DATE: 21-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0350001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 210 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-902-773A-4

Query Match 34.4%; Score 824.5; DB 10; Length 210;
 Best Local Similarity 88.8%; Pred. No. 4.1e-55;
 Matches 159; Conservative 4; Mismatches 15; Indels 1; Gaps 1;
 QY 254 GRGDSPASSKPIISINRYEIDKPSMAAGSITTLPALPEDGSGAFPPGHFKDPKRLCYCKN 313
 Db 33 GRGTAAPRAAPAAFGARSRG-PAGTMAAGSITTLPALPEDGSGAFPPGHFKDPKRLCYCKN 91
 QY 314 GFFLRHDPDGVDRGVRKSDPHIKLOLAERGVVSIKVCANRYLAMKEDGRLLASKCV 373
 Db 92 GFFLRHDPDGVDRGVRKSDPHIKLOLAERGVVSIKVCANRYLAMKEDGRLLASKCV 151
 QY 374 VTDECFEFLRLESNNYNTYRSRKYTSWYVALKRTGQYKLGSGTGOKAILFLPMSAAS 432
 Db 152 VTDECFEFLRLESNNYNTYRSRKYTSWYVALKRTGQYKLGSGTGOKAILFLPMSAAS 210

RESULT 3
 US-09-826-210-2
 ; Sequence 2, Application US/09826210
 ; Patent No. US20010020004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Springer, Barry A.
 ; APPLICANT: Pantoliano, Michael W.
 ; APPLICANT: Sharp, Celia M.
 ; TITLE OF INVENTION: Analogs of Human basic Fibroblast Growth Factor
 ; FILE REFERENCE: 1503.0220003
 ; CURRENT APPLICATION NUMBER: US/09/826,210
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US 09/220,077
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 60/068,667
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent In Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-210-2

Query Match 34.2%; Score 821; DB 10; Length 158;
 Best Local Similarity 98.7%; Pred. No. 5.1e-55;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 277 SMAAGSITTLPALPEDGSGAFPPGHFKDPKRLCYCKNGFFLRHDPDGVDRGVRKSDPH 336
 Db 3 TMAAGSITTLPALPEDGSGAFPPGHFKDPKRLCYCKNGFFLRHDPDGVDRGVRKSDPH 62
 QY 337 IKLOLAERGVVSIKVCANRYLAMKEDGRLLASKCVTDECFEFLRLESNNYNTYRSRK 396
 Db 63 IKLOLAERGVVSIKVCANRYLAMKEDGRLLASKCVTDECFEFLRLESNNYNTYRSRK 122
 QY 397 YTSWYVALKRTGQYKLGSGTGOKAILFLPMSAAS 432
 Db 123 YTSWYVALKRTGQYKLGSGTGOKAILFLPMSAAS 158

RESULT 4
 US-10-081-347-28
 ; Sequence 28, Application US/10081347
 ; Publication No. US2003008351A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Delisher, Theresa A.
 ; APPLICANT: Conklin, Darrell C.
 ; APPLICANT: Raymond, Fenella
 ; APPLICANT: Bukowski, Thomas R.
 ; APPLICANT: Holdeman, Susan D.
 ; APPLICANT: Hansen, Brigit O.
 ; APPLICANT: Sheppard, Paul O.
 ; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
 ; FILE REFERENCE: 96-20C1
 ; CURRENT APPLICATION NUMBER: US/10/081,347
 ; CURRENT FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: US/09/229,947
 ; PRIOR FILING DATE: 1999-01-13
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 28
 ; LENGTH: 155
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-081-347-28

Query Match 34.2%; Score 820; DB 9; Length 155;
 Best Local Similarity 99.4%; Pred. No. 5.9e-55;
 Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHFKDKRLCYCKNGFFLRHHPDGRVDGVREKSDPHI 337

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Db 1 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 120
QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAKS 155
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RESULT 8
US-09-251-263-10
; Sequence 10, Application US/09251263
; Patent No. US20020052477A1
; GENERAL INFORMATION:
; APPLICANT: Mathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; FILE REFERENCE: 07265/047003
; CURRENT APPLICATION NUMBER: US/09/251,263
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 08/867,471
; EARLIER FILING DATE: 1997-06-02
; EARLIER APPLICATION NUMBER: 08/439,725
; EARLIER FILING DATE: 1995-05-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-251-263-10
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Query Match 34.2%; Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 337
Db 1 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 120
QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAKS 155
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```
RESULT 9
US-09-425-021-10
; Sequence 10, Application US/09425021
; Patent No. US20020076748A1
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PF20301
; CURRENT APPLICATION NUMBER: US/09/425,021
; EARLIER FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 09/103,079
; EARLIER FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-425-021-10
Query Match 34.2%; Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 337
Db 1 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 120
QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAKS 155
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RESULT 10
US-09-886-856-8
; Sequence 8, Application US/09886856
; Patent No. US20020115603A1
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha Jo
; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Treatment of Peripheral Artery Disease
; FILE REFERENCE: PPI6090.004
; CURRENT APPLICATION NUMBER: US/09/886,856
; EARLIER FILING DATE: 2001-06-21
; EARLIER APPLICATION NUMBER: 60/213,504
; EARLIER FILING DATE: 2000-06-22
; EARLIER APPLICATION NUMBER: 60/264,572
; EARLIER FILING DATE: 2000-01-26
; EARLIER APPLICATION NUMBER: 60/276,549
; EARLIER FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-856-8
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Query Match 34.2%; Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 337
Db 1 MAAGSTTLPALPEDGSGAFPFGHFKDPKRLCKNGGFFLRHHPDGRVDGVRKSDPHI 60
QY 338 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 397
Db 61 KIOLAEEERGVSIGVCANRYLAMKEDGRLASCKVTECEFFERLESNNNTYRSRKY 120
QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
Db 121 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAKS 155
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RESULT 11
US-09-749-728B-7
; Sequence 7, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihito
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Ogawa, Keiichi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
```

```

: TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
: FILE REFERENCE: 00766.000043
: CURRENT APPLICATION NUMBER: US/09/749,728B
: CURRENT FILING DATE: 2001-09-17
: PRIOR APPLICATION NUMBER: H11-372826
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: PCT-JP00-01148
: PRIOR FILING DATE: 2000-02-28
: PRIOR APPLICATION NUMBER: PCT-JP00-07741
: PRIOR FILING DATE: 2000-11-02
: NUMBER OF SEQ ID NOS: 80
: SOFTWARE: PatentIn Ver.2.0
: SEQ ID NO 7
: LENGTH: 155
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-749-728B-7

Query Match          34.2% Score 820; DB 10; Length 155;
Best Local Similarity 99.4%; Pred. No. 5.9e-55;
Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFELRIHPDGRVGVREKSDPHI 337
DB 1 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFELRIHPDGRVGVREKSDPHI 60

QY 338 KLOLQAEERGVVSIGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNNTYRSRY 397
DB 61 KLOLQAEERGVVSIGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNNTYRSRY 120

QY 398 TSMYVALKRTGYKLGSKTGPCKAILFLPMSAAS 432
DB 121 TSMYVALKRTGYKLGSKTGPCKAILFLPMSAKS 155

RESULT 12
US-09-934-706-2
: Sequence 2, Application US/09934706
: Patent No. US20020102709A1
: GENERAL INFORMATION:
: APPLICANT: Terumo Corporation
: TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
: FILE REFERENCE: 19990120
: CURRENT APPLICATION NUMBER: US/09/934,706
: CURRENT FILING DATE: 2001-08-23
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE:
: SEQ ID NO 2
: LENGTH: 159
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Human Basic
: OTHER INFORMATION: Fibroblast Growth Factor with Enterokinase
: OTHER INFORMATION: Recognition Sequence
: NAME/KEY: PEPTIDE
: LOCATION: (1)..(5)
: OTHER INFORMATION: /note="enterokinase recognition sequence"
: NAME/KEY: PEPTIDE
: LOCATION: (6)..(159)
: OTHER INFORMATION: /note="human fibroblast growth factor"
: US-09-934-706-2

Query Match          34.1% Score 818; DB 10; Length 159;
Best Local Similarity 96.9%; Pred. No. 8.6e-55;
Matches 154; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 274 DKPSMAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFELRIHPDGRVGVREKS 333
DB 1 DDDDKMAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFELRIHPDGRVGVREKS 60

QY 334 DPHIKIQLQAEERGVVSIGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNNTYR 393
```

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DB 61 DPHIKIQLQAEERGVVSIGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNNTYR 120

QY 394 SRKYSWYVALKRTGYKLGSKTGPCKAILFLPMSAAS 432
DB 121 SRKYSWYVALKRTGYKLGSKTGPCKAILFLPMSAKS 159

RESULT 13
US-10-108-195-1
: Sequence 1, Application US/10108195
: Publication No. US20030008820A1
: GENERAL INFORMATION:
: APPLICANT: Kwan, Chi-Pong
: APPLICANT: Venkataraman, Ganesh
: APPLICANT: Shriver, Zachary
: APPLICANT: Raman, Rahul
: APPLICANT: Sasisekharan, Ram
: TITLE OF INVENTION: Methods and Products Related to FGF Dimerization
: FILE REFERENCE: M00656/7/0076
: CURRENT APPLICATION NUMBER: US/10/108,195
: CURRENT FILING DATE: 2002-03-27
: PRIOR APPLICATION NUMBER: US 60/279,165
: PRIOR FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 155
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-108-195-1

Query Match          33.9% Score 814; DB 9; Length 155;
Best Local Similarity 98.7%; Pred. No. 1.7e-54;
Matches 153; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 278 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFELRIHPDGRVGVREKSDPHI 337
DB 1 MAAGSITTLPALPEDGSGAFPFGHFKDPKRLCKNGGFELRIHPDGRVGVREKSDPHI 60

QY 338 KLOLQAEERGVVSIGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNNTYRSRY 397
DB 61 KLOLQAEERGVVSIGVCANRYLAMKEDGRLLASKCVTDECFEERLESNNNTYRSRY 120

QY 398 TSMYVALKRTGYKLGSKTGPCKAILFLPMSAAS 432
DB 121 TSMYVALKRTGYKLGSKTGPCKAILFLPMSAKS 155

RESULT 14
US-09-802-365-6
: Sequence 6, Application US/09802365
: Patent No. US20020032153A1
: GENERAL INFORMATION:
: APPLICANT: Whitehouse, Martha Jo
: TITLE OF INVENTION: Methods and Compositions for the
: FILE REFERENCE: 1671.003
: CURRENT APPLICATION NUMBER: US/09/802,365
: CURRENT FILING DATE: 2001-03-09
: PRIOR APPLICATION NUMBER: 60/188,480
: PRIOR FILING DATE: 2000-03-10
: PRIOR APPLICATION NUMBER: 60/203,415
: PRIOR FILING DATE: 2000-05-11
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 155
: TYPE: PRT
: ORGANISM: Bos taurus
: US-09-802-365-6

Query Match          33.8% Score 811; DB 10; Length 155;
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Best Local Similarity 98.1%; Pred. No. 2.8e-54;
Matches 152; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 278 MAGSITTLPALPEDGSGAFPPGHFKDPKRLCKNGGFFLRHPDGRVDGVREKSDPHI 337
Db 1 MAGSITTLPALPEDGSGAFPPGHFKDPKRLCKNGGFFLRHPDGRVDGVREKSDPHI 60
OY 338 KLOLQAEERGVSIVKVCANRYLAMKEDGRLASKCVTDECFFERLESNNYTYRSRKY 397
Db 61 KLOLQAEERGVSIVKVCANRYLAMKEDGRLASKCVTDECFFERLESNNYTYRSRKY 120
OY 398 TSWYVALKRTGOKLGTGPGOKALFLPMSAKS 432
Db 121 TSWYVALKRTGOKLGTGPGOKALFLPMSAKS 155

RESULT 15

US-09-886-856-6
Sequence 6, Application US/09886856
Patent No. US20020115603A1

GENERAL INFORMATION:

APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions for the
FILE REFERENCE: Pp16090.004
CURRENT APPLICATION NUMBER: US/09/886,856
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,504
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/264,572
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/276,549
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 155
TYPE: PRT
ORGANISM: Bos taurus
US-09-886-856-6

Query Match 33.8%; Score 811; DB 10; Length 155;
Best Local Similarity 98.1%; Pred. No. 2.8e-54;
Matches 152; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 278 MAGSITTLPALPEDGSGAFPPGHFKDPKRLCKNGGFFLRHPDGRVDGVREKSDPHI 337
Db 1 MAGSITTLPALPEDGSGAFPPGHFKDPKRLCKNGGFFLRHPDGRVDGVREKSDPHI 60
OY 338 KLOLQAEERGVSIVKVCANRYLAMKEDGRLASKCVTDECFFERLESNNYTYRSRKY 397
Db 61 KLOLQAEERGVSIVKVCANRYLAMKEDGRLASKCVTDECFFERLESNNYTYRSRKY 120
OY 398 TSWYVALKRTGOKLGTGPGOKALFLPMSAKS 432
Db 121 TSWYVALKRTGOKLGTGPGOKALFLPMSAKS 155

Search completed: March 13, 2003, 11:36:40
Job time : 27 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 07:34:37 ; Search time 39 Seconds
(without alignments)
1126.498 Million cell updates/sec

Title: US-09-775-964-5
Perfect score: 2398
Sequence: 1 PTDLRFTNIGPDMRTWAP.....LVTLPHNLHGPEILDVST 457

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_73:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 1474 | 61.5 | 2386 | 1 FNMU | fibronectin precu |
| 2 | 1396 | 58.2 | 2265 | 1 FNBO | fibronectin - bov |
| 3 | 1345 | 56.1 | 2477 | 2 S14428 | fibronectin precu |
| 4 | 1018.5 | 42.5 | 2481 | 2 A43908 | fibronectin - Affi |
| 5 | 848 | 35.4 | 273 | 2 A28512 | fibronectin - chic |
| 6 | 824.5 | 34.4 | 210 | 2 A32398 | basic fibroblast g |
| 7 | 812 | 33.9 | 157 | 1 GKBOB | basic fibroblast g |
| 8 | 792.5 | 33.0 | 154 | 2 A31674 | basic fibroblast g |
| 9 | 777.5 | 32.4 | 154 | 2 C37360 | basic fibroblast g |
| 10 | 768 | 32.0 | 189 | 2 S71465 | fibronectin - chic |
| 11 | 764 | 31.9 | 146 | 1 S00185 | basic fibroblast g |
| 12 | 754.5 | 31.5 | 164 | 2 S31622 | basic fibroblast g |
| 13 | 753 | 31.4 | 189 | 2 A48834 | basic fibroblast g |
| 14 | 738 | 30.8 | 137 | 2 I46711 | fibroblast growth |
| 15 | 681 | 28.4 | 155 | 1 A40117 | basic fibroblast g |
| 16 | 613.5 | 25.6 | 1020 | 2 A29355 | fibronectin - chic |
| 17 | 467 | 19.5 | 125 | 2 A32484 | basic fibroblast g |
| 18 | 425.5 | 17.7 | 155 | 1 A60721 | acidic fibroblast |
| 19 | 417.5 | 17.4 | 155 | 2 A60130 | acidic fibroblast |
| 20 | 416.5 | 17.4 | 155 | 1 A33665 | acidic fibroblast |
| 21 | 411.5 | 17.2 | 155 | 2 S04147 | acidic fibroblast |
| 22 | 411.5 | 17.2 | 155 | 2 D37360 | acidic fibroblast |
| 23 | 403.5 | 16.8 | 152 | 2 JH0476 | acidic fibroblast |
| 24 | 402.5 | 16.8 | 155 | 2 JH0055 | acidic fibroblast |
| 25 | 400.5 | 16.7 | 155 | 1 GKBOA | acidic fibroblast |
| 26 | 378.5 | 15.8 | 1356 | 2 A45445 | Janusin precursor, |
| 27 | 358 | 14.9 | 1353 | 2 JH0675 | restriotin precus |
| 28 | 338.5 | 14.1 | 1746 | 1 S19694 | tenascin precursor |
| 29 | 334.5 | 13.9 | 2201 | 2 A32160 | tenascin-C - human |

| | | | | | |
|----|-------|------|------|----------|--------------------|
| 30 | 333.5 | 13.9 | 929 | 2 I51027 | type XII collagen |
| 31 | 329 | 13.7 | 1810 | 1 A32230 | tenascin precursor |
| 32 | 327 | 13.6 | 2019 | 1 J01322 | tenascin precursor |
| 33 | 309 | 12.9 | 3124 | 1 A40020 | collagen alpha 1(X |
| 34 | 302.5 | 12.6 | 4135 | 2 T42629 | collagen alpha 1(X |
| 35 | 297.5 | 12.4 | 843 | 2 A40970 | undulin 1 - human |
| 36 | 290.5 | 12.1 | 1857 | 2 S31212 | collagen alpha 1(X |
| 37 | 290.5 | 12.1 | 1888 | 2 S78476 | collagen alpha 1(X |
| 38 | 289.5 | 12.1 | 1747 | 1 A45974 | collagen alpha 1(X |
| 39 | 280.5 | 11.7 | 933 | 2 A31930 | cytotactin - chick |
| 40 | 275.5 | 11.5 | 3566 | 1 A40701 | tenascin-X precurs |
| 41 | 274 | 11.4 | 860 | 2 I48839 | tenascin-X - mouse |
| 42 | 274 | 11.4 | 4006 | 2 T09070 | probable tenascin |
| 43 | 272 | 11.3 | 2944 | 2 A54849 | collagen alpha 1(V |
| 44 | 270.5 | 11.3 | 206 | 1 TVDHHS | fibroblast growth |
| 45 | 266 | 11.1 | 194 | 2 I50710 | fibroblast growth |

ALIGNMENTS

RESULT 1
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fibronectin precursor [validated] - human
N:Alternate names: fibronectin splice form ED-A
C:Species: Homo sapiens (man)
C:Date: 27-Nov-1985 #sequence:revision 31-Mar-1993 #ext-change 08-Dec-2000
C:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495;
R:Dean, D.C.; Bowlin, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A:Reference number: A26460; MUID:87175578; PMID:3031656
A:Accession: A26460
A:Molecule type: DNA
A:Residues: 1-49 <DEA>
A:Cross-references: GB:M15801; NID:9182686; PIDN:AAAS376.1; PID:9553293
R:Oldberg, A.; Ruoslahti, E.
J. Biol. Chem. 261, 2113-2116, 1986
A:Title: Evolution of the fibronectin gene.
A:Reference number: A26284; MUID:86111901; PMID:3003095
A:Accession: A26284
A:Molecule type: DNA
A:Residues: 1447-1540 <OLD>
A:Cross-references: GB:M12549; NID:9182688
A:Note: the authors translated the codon TTC for residue 1494 as Glu
Nucleic Acids Res. 16, 3545-3557, 1988
A:Title: Sequence analysis and in vivo expression show that alternative splicing of E
A:Reference number: S00848; MUID:88233940; PMID:3375063
A:Accession: S03917
A:Molecule type: DNA
A:Residues: 1594-1767, /V/, 1769-1783 <PAO>
A:Cross-references: EMBL:X07718; NID:931402
A:Note: the authors translated the codon AAC for residue 1631 as Asp
FEBS Lett. 207, 287-291, 1986
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin ge
A:Reference number: A24854; MUID:87030929; PMID:3770201
A:Accession: A24854
A:Molecule type: DNA
A:Residues: 1992-2147 <VIB>
A:Cross-references: GB:X04530; NID:931436
R:Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.
A:Reference number: A24476; MUID:87030890; PMID:3770189
A:Accession: A24476
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-14, /Q/, 16-38 <GUT>
R:Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A:Title: Primary structure of human fibronectin: differential splicing may generate a

A:Reference number: A91008; MUID:85284965; PMID:2992933
A:Accession: A91008
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 32-1344,1346-2080,2112-2386 <KOR>
A:Cross-references: GB:X02761
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5866, 1984
A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A:Reference number: A93529; MUID:84272258; PMID:6462919
A:Accession: A93529
A:Molecule type: mRNA
A:Residues: 973-2080,2112-2386 <K02>
A:Cross-references: GB:X00739
R:Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell
A:Reference number: A21011; MUID:83290929; PMID:6688418
A:Accession: A21011
A:Molecule type: mRNA
A:Residues: 1434-1537 <OT2>
A:Cross-references: GB:K00055; NID:9182680; PIDN:AAA52459.1; PID:9182683
R:Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with re
A:Reference number: A90495; MUID:85280409; PMID:2992573
A:Accession: A90495
A:Molecule type: mRNA
A:Residues: 1594-2386 <BER>
A:Cross-references: GB:M10905; NID:9182696; PIDN:AAA52462.1; PID:9182697
R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A:Reference number: A22245; MUID:85231203; PMID:2989004
A:Accession: A22245
A:Molecule type: mRNA
A:Residues: 1948-2067 <UM2>
A:Cross-references: GB:M27589; NID:9182705; PIDN:AAA52465.1; PID:9182706
A:Accession: B22245
A:Molecule type: mRNA
A:Residues: 1975-1991,2017-2039 <UM2>
A:Cross-references: GB:M27590
R:Seikiguchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A:Title: Human liver fibronectin complementary DNAs: identification of two different mes
A:Reference number: I52394; MUID:87026578; PMID:3021206
A:Accession: I52394
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1978-1990,2016-2018, 'N', 2020-2081,2113-2127 <SER>
A:Cross-references: GB:M14060; NID:9182701; PIDN:AAA52464.1; PID:9182704
R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
A:Reference number: A21165; MUID:83221567; PMID:6304699
A:Accession: A21165
A:Molecule type: mRNA
A:Residues: 2291-2386 <K03>
A:Cross-references: GB:K00799; NID:9182681; PIDN:AAA52460.1; PID:9182684
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A:Title: Primary structure of human plasma fibronectin.
A:Reference number: A92398; MUID:84032463; PMID:6630202
A:Accession: A92398
A:Molecule type: Protein
A:Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R:Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A:Title: Further characterization of the binding of fibronectin to gelatin reveals the F
A:Reference number: S34791; MUID:93312001; PMID:8323285
A:Accession: S34791
A:Molecule type: Protein
A:Residues: 291-300,551-560 <GAR2>

R:Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A:Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A:Reference number: A60904; MUID:87019725; PMID:3532418
A:Accession: A60904
A:Molecule type: Protein
A:Residues: 293-301 <GR1>
R:Calaycay, J.; Pardo, H.; Lee, T.; Borsl, L.; Sirl, A.; Shively, J.E.; Zardl, L.
J. Biol. Chem. 260, 12136-12141, 1985
A:Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human
A:Reference number: A23901; MUID:86008277; PMID:3900070
A:Accession: A23901
A:Molecule type: Protein
A:Residues: 616-677, 'O', 679-703, 'PR' <CAT>
R:Pierschbacher, M.D.; Ruoslahti, E.; Sundell, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A:Title: The cell attachment domain of fibronectin. Determination of the primary stru
A:Reference number: A92386; MUID:82265604; PMID:7050098
A:Accession: A92386
A:Molecule type: Protein
A:Residues: 1441-1548 <PIE>
A:Note: Residues 1524-1527 are responsible for the cell-binding activity
R:Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A:Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa
A:Reference number: A32517; MUID:87241275; PMID:3593230
A:Accession: A32517
A:Molecule type: Protein
A:Residues: 1589-1630, 'T', 1722-2058 <GAR3>
R:Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; P
Biochem. J. 274, 731-738, 1991
A:Title: Human plasma fibronectin. Demonstration of structural differences between th
A:Reference number: S14357; MUID:91190085; PMID:2012601
A:Accession: S14357
A:Molecule type: Protein
A:Residues: 1614-1630, 'T', 1722-2081,2113-2244 <PRE>
R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A:Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-
A:Reference number: A23891; MUID:85261459; PMID:4019516
A:Accession: A23891
A:Molecule type: Protein
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C:Comment: The cellular and plasma fibronectins are high molecular weight glycoprotei
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A:Gene: GDB:FNI
A:Cross-references: GDB:119135; OMIM:135600
A:Map position: 2q34-2q34
A:Introns: 49/3; 1266/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145
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F:52-87/Domain: fibronectin type I repeat homology <1F2>
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F:141-179/Domain: fibronectin type I repeat homology <1F4>
F:186-225/Domain: fibronectin type I repeat homology <1F5>
F:231-270/Domain: fibronectin type I repeat homology <1F6>
F:308-342/Domain: collagen binding <CBR>
F:308-342/Domain: fibronectin type I repeat homology <1F6>
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F:420-461/Domain: fibronectin type II repeat homology <2F2>
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F:518-555/Domain: fibronectin type I repeat homology <1F8>
F:561-599/Domain: fibronectin type I repeat homology <1F9>
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F:716-706/Domain: heparin binding <HBA>
F:719-801/Domain: fibronectin type III repeat homology <3F2>
F:810-891/Domain: fibronectin type III repeat homology <3F3>

F:906-888/Domain: fibronectin type III repeat homology <3FD>
 F:996-1077/Domain: fibronectin type III repeat homology <3FE>
 F:1086-1164/Domain: fibronectin type III repeat homology <3FE>
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Query Match 61.5%; Score 1474; DB 1; Length 2386;
 Best Local Similarity 46.8%; Pred. No. 5,6e-97;

Matches 351; Conservative 28; Mismatches 75; Indels 296; Gaps 17;

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QY 61 PGTEVVSVSVOHESTPLRGROKGLDPTGIDFSDITANSTVMIARATITGR 120
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Db 1330 PGTEVVSVSVOHESTPLRGROKGLDPTGIDFSDITANSTVMIARATITGR 1389
QY 121 IRHPEHSGRPREDRVHSHNSITLTLPTGTEVVSIVALNGRESPFLIGQSTVSD 180
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Db 1390 IRHPEHSGRPREDRVHSHNSITLTLPTGTEVVSIVALNGRESPFLIGQSTVSD 1449
QY 181 VPRDLEVAAPTSLISMDAPAVTVRYRTYGETGNSPVQETTPGSKSTATISGLK 240
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Db 1450 VPRDLEVAAPTSLISMDAPAVTVRYRTYGETGNSPVQETTPGSKSTATISGLK 1509
QY 241 PGVDTITVAVTGRGDSPASSKPSISNVRFEIDKPS-----M 278
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Db 1510 PGVDTITVAVTGRGDSPASSKPSISNVRFEIDKPSQMOVTVDNDSIVKMLDSSSPV 1569
QY 279 AAGSTITLP----- 287
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Db 1570 TGYRVTTPKNGPGTKTKTAGPQTEMTIEGLQPTVEVVSIVQNPBSGESQPLVQTA 1629
QY 288 -----ALPEDGSGGARP-PGHFKDPKRL 309
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Db 1630 TNIDRPKGLAFDVVDVDSIKIAMESPGQVSRVRYTSSPEDGIELHPAPDGEEDTAL 1689
QY 310 YCKNG-----FELRIH-----PDGVR 326
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Db 1690 QGLRPGSEYTVSVALHDMDMESQPLIGQSTAIAPPTDKTQVPTSLISAQWTPPNVQL 1749
QY 327 DGVR-----EKSDPHIKLOAEERGVSIKVCANRY-----LAMKEDGRILASK----- 372
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Db 1750 TGYRVRVPRKKEKTPKMKELNAPDSSSVVSGLMATKEVSVYALKD-----TLTSRPAAG 1806
QY 373 -----CVTDEC-----FFERLESNNVTYVS-----R 395
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Db 1807 VVTTLENVSPPRRAVTDATETTTITISWTKTETITGFGVDVAVPANGQTPRIORTIKPDVR 1866
QY 396 KYT-----SMVYA 403
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Db 1867 STTTGLGPGDYKIYLYTLNDNARSSPVYDASTAIDAPSNLRFPLATTPNSLVWSOPP 1926
QY 404 LKRTGOY-----KLGSK-----TG--PGKAILFL-----PM- 428
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Db 1987 GRKKTDELPLQVLTLPRLHGPILLDVPST 2016

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RESULT 2

FNBO
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 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 20-Oct-2000
 C:Accession: A26452; B21165; A23292
 R:Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
 Eur. J. Biochem. 161, 441-453, 1986
 A:Title: Complete primary structure of bovine plasma fibronectin.
 A:Reference number: A26452; MUID:87054047; PMID:3780752

A:Accession: A26452
 A:Molecule type: protein
 A:Residues: 1-2265 <SKO>
 R:Kornblith, A.R.; Vibbe-Pedersen, K.; Balle, F.E.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
 A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
 A:Reference number: A21165; MUID:83221567; PMID:6304699
 A:Accession: B21165
 A:Molecule type: mRNA
 A:Residues: 2170-2265 <KOR>
 A:Cross-references: GB:K00800; MID:9163055; PIDN:AAA30521.2; PID:95713323
 R:Petersen, T.E.; Thøgersen, H.C.; Skorstengaard, K.; Vibbe-Pedersen, K.; Sahl, P.; So
 Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
 A:Title: Partial primary structure of bovine plasma fibronectin: three types of inter
 A:Reference number: A23292; MUID:83117805; PMID:2215503
 A:Accession: A23292
 A:Molecule type: protein
 A:Residues: 1-16, 'C', 18-20, 'S', 22-432, 447-463, 1367-1517, 1567-1673, 2062-2176, 'N', 2178-
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 F:115-194/Domain: fibronectin type I repeat homology <1F3>
 F:200-239/Domain: fibronectin type I repeat homology <1F4>
 F:277-577/Domain: collagen binding <CBR>
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 F:66-104/Domain: fibronectin type I repeat homology <1F2>
 F:110-148/Domain: fibronectin type I repeat homology <1F3>
 F:155-194/Domain: fibronectin type I repeat homology <1F4>
 F:200-239/Domain: fibronectin type I repeat homology <1F5>
 F:277-577/Domain: collagen binding <CBR>
 F:277-311/Domain: fibronectin type I repeat homology <1F5>
 F:329-370/Domain: fibronectin type II repeat homology <2F1>
 F:389-430/Domain: fibronectin type II repeat homology <2F2>
 F:439-477/Domain: fibronectin type I repeat homology <1F7>
 F:487-524/Domain: fibronectin type I repeat homology <1F8>
 F:530-568/Domain: fibronectin type I repeat homology <1F9>
 F:578-661/Domain: fibronectin type III repeat homology <FN3A>
 F:688-770/Domain: fibronectin type III repeat homology <FN3B>
 F:779-860/Domain: fibronectin type III repeat homology <FN3C>
 F:875-957/Domain: fibronectin type III repeat homology <FN3D>
 F:965-1046/Domain: fibronectin type III repeat homology <FN3E>
 F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>
 F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>
 F:1235-1318/Domain: fibronectin type III repeat homology <FN3H>
 F:1326-1404/Domain: fibronectin type III repeat homology <GN31>
 F:1410-1517/Domain: cell attachment <CAD>
 F:1416-1502/Domain: fibronectin type III repeat homology <FN3J>
 F:1493-1495/Domain: cell attachment (R-G-D) motif
 F:1510-1592/Domain: fibronectin type III repeat homology <FN3K>
 F:1600-1670/Domain: heparin binding <HB2>
 F:1600-1682/Domain: fibronectin type III repeat homology <FN3L>
 F:1692-1773/Domain: fibronectin type III repeat homology <FN3M>
 F:1781-1863/Domain: fibronectin type III repeat homology <FN3N>
 F:1970-1972/Domain: cell attachment (R-G-D) motif
 F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>
 F:1985-2216/Domain: fibrin binding <FB2>
 F:2085-2124/Domain: fibronectin type I repeat homology <1F10>
 F:2130-2167/Domain: fibronectin type I repeat homology <1F11>
 F:2174-2209/Domain: fibronectin type I repeat homology <1F12>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Cross-link: isopeptide (Gln) (interchain to lys N6-amino of fibrin) #status exper
 F:21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,30
 F:399,497,511,846,976,1213,1987/Binding site: carboxylate (Asn) (covalent) #status e
 F:1205,1692/Binding site: carboxylate (Asn) (covalent) #status absent
 F:1943,1944/Binding site: carboxylate (His) (covalent) #status experimental
 F:2246/Disulfide bonds: interchain (to 2250) #status predicted
 F:2250/Disulfide bonds: interchain (to 2246) #status predicted
 F:2265/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match

58.2%; Score 1396; DB 1; Length 2265;

Best Local Similarity 48.6%; Pred. No. 2e-91;
Matches 327; Conservative 38; Mismatches 76; Indels 232; Gaps 17;

```

OY 1 PDDLRNTNIGPDMRYTAPPPSIDLTNELYRSPVKNEDVALSISPSDNAVLTNLT
DB 1239 PDDLRNTNIGPDMRYTAPPPSIDLTNELYRSPVKNEDVALSISPSDNAVLTNLT
OY 61 PGTETVYVSSVSEHSEHSPPLRGROKTGSDPTGIDPSDTTANSFTVHWIAPRAITTYGR
DB 1299 PGTETVYVSSVSEHSEHSPPLRGROKTGSDPTGIDPSDTTANSFTVHWIAPRAITTYGR
OY 121 IRRHHEPFGRRRDRRPPRSNITLTNLTPTGTEYVSVIALNGREPSPLIGQOSTVSD
DB 1359 IRRHHEPFGRRRDRRPPRSNITLTNLTPTGTEYVSVIALNGREPSPLIGQOSTVSD
OY 181 VPRDLVAVATPTSLISMDAPAVTVRYRITTYGEGTGSNPSVQETVPGSKSTATISGLK
DB 1419 VPRDLVAVATPTSLISMDAPAVTVRYRITTYGEGTGSNPSVQETVPGSKSTATISGLK
OY 241 PGVDYITVYAVTGRDSSPSSKPSISINRTETDKRPSMA-----AGSITTLPA-----
DB 1479 PGVDYITVYAVTGRDSSPSSKPSISINRTETDKRPSMA-----AGSITTLPA-----
OY 289 -----LPEDGSGAFPPGCHKRDK-----RLYCKN----- 313
DB 1539 TGVRYTAPKNG-----FGPSKTKTVGDQTEMTEGLQPTVEYVSVYAOQNGESQP 1592
OY 314 -----GGEFLRHDPGRVDGVRKSDPHI 337
DB 1593 LVQIVATTPAPTNLKTQVPTSLTAQWTAENVOLTGRRVTP-----KEKTPMK 1645
OY 338 KIQLOAEERGVSVKQVCANRY-----LANKEDGRLLASK-----CVT 375
DB 1646 EENLAPDSSSVVSGLMVATKYEVSVALKD-----TLTSRPAQGVVTTLENVSPRRARYT 1702
OY 376 DEC-----FFERLESNNY-----NTYRSRK 396
DB 1703 DATETTTISMTKTETITGQVDAIPANGQPTPIORTIRPDVRSYTTIGLQPTGTIHL 1762
OY 397 YT-----SWMVALKRTGOY-----KLGSK 415
DB 1763 YTLNDNANSSPVVIDASTAIDAPSNRLATTPNSLISWOPPRARITGYIIKKEPGSP 1822
OY 416 -----GG- PGCK-----AIIPLPSMAS-----DELQVLTLPHP 444
DB 1823 PREVPRRRPGVTEATITGLEGTETVTLQVIALKNQKSEPLIGRKKTDLPQVLTLPHP 1882
OY 445 NLHGEITIDVST 457
DB 1883 NLHGEITIDVST 1895

```

RESULT 3

SI4428 fibronectin precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Aug-1999

C:Accession: SI4428; SI2455; A22319; S46203; S00459; A27252; I59049

R:Hynes, R.O.
submitted to the EMBL Data Library, July 1989

A:Reference number: SI4428

A:Molecule type: mRNA

A:Residues: 1-2477 <HYN>

A:Cross-references: EMBL:X15906; NID:956163; PIDN:CAA34020.1; PID:956164

R:Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.

A:Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.

A:Reference number: SI2455; MUID:880549531; PMID:2445360

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 609-1810, 'T', 1812-2283 <SCH>

A:Cross-references: EMBL:X15906
R:Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A:Title: A single rat fibronectin gene generates three different mRNAs by alternative splicing
A:Reference number: A22319; MUID:84298097; PMID:6089177
A:Accession: A22319
A:Molecule type: DNA
A:Residues: 2052-2237 <TAM>
R:Palckenberg, C.; Engblid, J.J.; Thøgersen, I.B.; Salvesen, G.; Aketstroem, B.
Biochem. J. 301, 745-751, 1994
A:Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex
A:Reference number: S46203; MUID:94330948; PMID:7519849
A:Accession: S46203
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1183-1192; 'GLN', 1268, 'P', 1270-1271, 'D', 1273, 'CP', 1276, 'PV', 1385-1399 <PAL>
R:Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A:Title: Organization of the fibronectin gene provides evidence for exon shuffling du
A:Reference number: S00459; MUID:88054950; PMID:3119323
A:Accession: S00459
A:Molecule type: DNA
A:Residues: 1-139; 2382-2477 <PAT>
A:Cross-references: EMBL:X05831
A:Note: the authors translated the codon CCG for residues 51 and 94 as Ala
R:Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
Cell 35, 421-431, 1983
A:Title: Three different fibronectin mRNAs arise by alternative splicing within the c
A:Reference number: A27252; MUID:84082067; PMID:6317187
A:Accession: A27252
A:Molecule type: mRNA
A:Residues: 1586-1720, 'T', 1722, 1813-2477 <SCH>
R:Odermatt, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A:Title: Repeating modular structure of the fibronectin gene: Relationship to protein
A:Reference number: I59049; MUID:86016741; PMID:3863113
A:Accession: I59049
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1722-1810 <RES>
A:Cross-references: GB:M11750; NID:9204164; PIDN:AAA41170.1; PID:9554437
A:Genetics:
C:Introns: 51/1; 94/1; 2416/3; 2454/3
C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II r
C:Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; du
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-2477/Product: fibronectin #status predicted <MAT>
F:53-88/Domain: fibronectin type I repeat homology <1F1>
F:98-136/Domain: fibronectin type I repeat homology <1F2>
F:142-180/Domain: fibronectin type I repeat homology <1F3>
F:187-226/Domain: fibronectin type I repeat homology <1F4>
F:232-271/Domain: fibronectin type I repeat homology <1F5>
F:308-342/Domain: fibronectin type I repeat homology <1F6>
F:360-401/Domain: fibronectin type II repeat homology <2F1>
F:420-461/Domain: fibronectin type II repeat homology <2F2>
F:470-508/Domain: fibronectin type I repeat homology <1F7>
F:518-555/Domain: fibronectin type I repeat homology <1F8>
F:561-599/Domain: fibronectin type I repeat homology <1F9>
F:609-637/Domain: fibronectin type I repeat homology <1F10>
F:659-697/Domain: fibronectin type III repeat homology <FN3A>
F:718-800/Domain: fibronectin type III repeat homology <FN3B>
F:809-890/Domain: fibronectin type III repeat homology <FN3C>
F:905-987/Domain: fibronectin type III repeat homology <FN3D>
F:992-1076/Domain: fibronectin type III repeat homology <FN3E>
F:1085-1164/Domain: fibronectin type III repeat homology <FN3F>
F:1172-1257/Domain: fibronectin type III repeat homology <FN3G>
F:1285-1348/Domain: fibronectin type III repeat homology <FN3H>
F:1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F:1447-1529/Domain: fibronectin type III repeat homology <FN3J>
F:1537-1619/Domain: fibronectin type III repeat homology <FN3K>
F:1614-1616/Region: cell attachment (R-G-D) motif
F:1631-1713/Region: fibronectin type III repeat homology <FN3L>
F:1721-1803/Domain: fibronectin type III repeat homology <FN3M>
F:1811-1893/Domain: fibronectin type III repeat homology <FN3N>

F:1903-1984/Domain: fibronectin type III repeat homology <FN30>
 F:1992-2074/Domain: fibronectin type III repeat homology <FN3>
 F:2181-2183/Region: cell attachment (R-G-D) motif
 F:2193-2273/Domain: fibronectin type III repeat homology <FN30>
 F:2296-2335/Domain: fibronectin type I repeat homology <FI10>
 F:2341-2378/Domain: fibronectin type I repeat homology <FI11>
 F:2385-2420/Domain: fibronectin type I repeat homology <FI12>
 F:53-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 232-261, 259-271, 308-335, 333
 368, 2366-2378, 2385-2411, 2409-2420/Disulfide bonds: #status predicted
 F:2458/Disulfide bonds: Interchain (to 2462) #status predicted
 F:2462/Disulfide bonds: Interchain (to 2458) #status predicted

Query Match 56.1%; Score 1345; DB 2; Length 2477;
 Best Local Similarity 42.4%; Pred. No. 1e-87;
 Matches 318; Conservative 49; Mismatches 87; Indels 296; Gaps 18;

QY 1 PTDLFTNIGPDYTMRYTMAPPSIDLTNFLVRSYSPVKNEDVAELISPSDNAVLTNLL 60
 Db 1360 PTDLFTNIGPDYTMRYTMAPPSIDLTNFLVRSYSPVKNEDVAELISPSDNAVLTNLL 1419
 / 61 PGTENVVSSVYEQHESTPLRGROKTDGSDTGDIDFSITANSFTVHVIARATITGYR 120
 Db 1420 PGTENVVSSVYEQHESTPLRGROKTDGSDTGDIDFSITANSFTVHVIARATITGYR 1479
 QY 121 IRHHEHFGSGRPREDVRPHSRNSITLTNLTPTGEVVSIVALNGRESPLLIGQOSTVSD 180
 Db 1480 IRHHEHFGSGRPREDVRPHSRNSITLTNLTPTGEVVSIVALNGRESPLLIGQOSTVSD 1539
 QY 181 VRDLEVVAAFPSTLLISMDAPAVTRYRYRITYGETGNSPVOEFTVPGSKSTATISGLK 240
 Db 1540 VRDLEVVAAFPSTLLISMDAPAVTRYRYRITYGETGNSPVOEFTVPGSKSTATISGLK 1599
 QY 241 PGVDYTIIVYAVTNGRDSPASSKPSISINRTETDKP-----M 278
 Db 1600 PGVDYTIIVYAVTNGRDSPASSKPSISINRTETDKP-----M 1659
 QY 279 AAGSTTLP----- 287
 Db 1660 TGYRTTAPKNGLGPTKSGTSPDQTEMTIEGLQPTVEVVSVAQNKGESQPLVQTA 1719
 QY 288 -----ALPEDGSGAP-PGHFKDPKRL 309
 Db 1720 TNDIRPKGLAFTDQVDSIKIMESPOGVSRYRYTSSPEDGIMELFPAPGDEDTABL 1779
 QY 310 Y-----CKNGSF-----FLRIH-----PDGRV 326
 Db 1780 HOLRPGSEYTSVVALHGMESQPLIGVOSTAIPAPTNLKTQVSPFTTLTAQMTAPSVKL 1839
 Y 327 DQVR-----EKSDPHIKLQLOAERGVVSINVCANRY-----LAMKEDGRLLASK- 372
 Db 1840 TGYRVVTPKKEKTPMKKEINLSPDSTSVIVSGLMATAKYEVSVALKD---TLTSRPAQ 1896
 QY 373 -----CYTDEC-----FFERLESNNY----- 389
 Db 1897 VVTTLENNSPRRARYTATETTTITISMRTKETITIGFOVDAIPANGQTPVORTISPDVR 1956
 QY 390 -----NTYRSKRYA-----SMVYA 403
 Db 1957 SYTTIGLOPCTDYKILHLYTLNDNANSSPVVIDASTAIDAPSMURFLTTPNSLLVSWQAP 2016
 QY 404 LKRTGOY-----KLGSK-----TG--PGKAILFL-----PM- 428
 Db 2017 RARITGILIKYEKPGSPREVPVRPRPGVTEATITIGLEPGTEYTIIVALKNNQKSEPLI 2076
 QY 429 -SAASDELQVLTLPHPNLHGPETIDVPST 457
 Db 2077 GRKKTDLPOLVTLPHPLHGPETIDVPST 2106

RESULT 4
 AA3908
 fibronectin - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Feb-1999
 C:Accession: AA3908
 R:DesImone, D.W.; Norton, P.A.; Hynes, R.O.
 Dev. Biol. 149, 357-369, 1992
 A:Title: Identification and characterization of alternatively spliced fibronectin mRNA
 A:Reference number: AA3908; MUID:92111942; PMID:1730390
 A:Accession: AA3908

A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-2481 <DES>
 A:Cross-References: GB:M77820

A>Note: sequence extracted from NCBI backbone (NCBI:77473)

C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II r

C:Keywords: duplication; extracellular matrix; glycoprotein; heterodimer

F:55-90/Domain: fibronectin type I repeat homology <FI1>
 F:100-138/Domain: fibronectin type I repeat homology <FI2>
 F:144-182/Domain: fibronectin type I repeat homology <FI3>
 F:189-228/Domain: fibronectin type I repeat homology <FI4>
 F:234-273/Domain: fibronectin type I repeat homology <FI5>
 F:309-343/Domain: fibronectin type I repeat homology <FI6>
 F:361-402/Domain: fibronectin type II repeat homology <FI1>
 F:421-462/Domain: fibronectin type II repeat homology <FI2>
 F:471-509/Domain: fibronectin type II repeat homology <FI3>
 F:519-556/Domain: fibronectin type I repeat homology <FI7>
 F:562-600/Domain: fibronectin type I repeat homology <FI8>
 F:610-693/Domain: fibronectin type I repeat homology <FI9>
 F:719-801/Domain: fibronectin type III repeat homology <FN3A>
 F:810-891/Domain: fibronectin type III repeat homology <FN3B>
 F:906-988/Domain: fibronectin type III repeat homology <FN3C>
 F:996-1077/Domain: fibronectin type III repeat homology <FN3D>
 F:1086-1165/Domain: fibronectin type III repeat homology <FN3E>
 F:1173-1258/Domain: fibronectin type III repeat homology <FN3F>
 F:1266-1349/Domain: fibronectin type III repeat homology <FN3G>
 F:1357-1440/Domain: fibronectin type III repeat homology <FN3H>
 F:1448-1530/Domain: fibronectin type III repeat homology <FN3I>
 F:1538-1620/Domain: fibronectin type III repeat homology <FN3J>
 F:1615-1617/Region: cell attachment (R-G-D) motif
 F:1633-1714/Domain: fibronectin type III repeat homology <FN3L>
 F:1722-1804/Domain: fibronectin type III repeat homology <FN3M>
 F:1812-1894/Domain: fibronectin type III repeat homology <FN3N>
 F:1904-1985/Domain: fibronectin type III repeat homology <FN3O>
 F:1993-2075/Domain: fibronectin type III repeat homology <FN3P>
 F:2197-2277/Domain: fibronectin type III repeat homology <FN3Q>
 F:2301-2340/Domain: fibronectin type I repeat homology <FI10>
 F:2346-2383/Domain: fibronectin type I repeat homology <FI11>
 F:2390-2425/Domain: fibronectin type I repeat homology <FI12>
 F:55-81, 79-90, 100-128, 126-138, 144-172, 170-182, 189-218, 216-228, 234-263, 261-273, 309-336, 2373, 2371-2383, 2390-2416, 2414-2425/Disulfide bonds: #status predicted
 F:2459/Disulfide bonds: Interchain (to 2463) #status predicted
 F:2463/Disulfide bonds: Interchain (to 2459) #status predicted

Query Match 42.5%; Score 1018.5; DB 2; Length 2481;
 Best Local Similarity 68.7%; Pred. No. 2.6e-64;
 Matches 195; Conservative 43; Mismatches 65; Indels 1; Gaps 1;

QY 1 PTDLFTNIGPDYTMRYTMAPPSIDLTNFLVRSYSPVKNEDVAELISPSDNAVLTNLL 60
 Db 1361 PTDLFTNIGPDYTMRYTMAPPSIDLTNFLVRSYSPVKNEDVAELISPSDNAVLTNLL 1420
 QY 61 PGTENVVSSVYEQHESTPLRGROKTDGSDTGDIDFSITANSFTVHVIARATITGYR 120
 Db 1421 PGTENVVSSVYEQHESTPLRGROKTDGSDTGDIDFSITANSFTVHVIARATITGYR 1480
 QY 121 IRHHEHFGSGRPREDVRPHSRNSITLTNLTPTGEVVSIVALNGRESPLLIGQOSTVSD 180
 Db 1481 IRHHEHFGSGRPREDVRPHSRNSITLTNLTPTGEVVSIVALNGRESPLLIGQOSTVSD 1540
 QY 181 VRDLEVVAAFPSTLLISMDAPAVTRYRYRITYGETGNSPVOEFTVPGSKSTATISGLK 240
 Db 1541 VRDLEVVAAFPSTLLISMDAPAVTRYRYRITYGETGNSPVOEFTVPGSKSTATISGLK 1600

Db 1601 PGVSITITVAVTGRGDSPPASSKPLTIHKTDVDPIDMAVTDI 1644

RESULT 5

A28512 fibronectin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Aug-1999

C:Accession: A28512

R:Kubomura, S.; Obata, M.; Kaseyaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K.

Biochem. Biophys. Acta 910, 171-181, 1987

A:Title: Genetic analysis of the cell binding domain region of the chicken fibronectin g

A:Reference number: A28512; MUID:88050950; PMID:2823899

A:Accession: A28512

A:Molecule type: DNA

A:Residues: 1-273 <KUR>

A:Cross-references: GB:J06553; NID:963393; PIDN:CAA29781.1; PID:9295716

A:Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243

C:Genetics: 90/1: 129/1: 184/1: 236/1

Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe

Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter

E:1-82/Domain: fibronectin type III repeat homology <FN3I>

F:1-90/172/Domain: fibronectin type III repeat homology <FN3J>

F:167-169/Region: cell attachment (R-G-D) motif

F:184-266/Domain: fibronectin type III repeat homology <FN3K>

Query Match 35.4% Score 848; DB 2; Length 273;

Best Local Similarity 84.7% Pred. No. 1.9e-53;

Matches 160; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 89 LDSPGTGDSIDITANSTFTVWIMAPRTITGYRIRHHPHSGSPRRDRVHNSITLTN 148

Db 1 LDSPGTGDSIDITANSTFTVWIMAPRTITGYRIRHHPHSGSPRRDRVHNSITLTN 60

QY 149 LTFGTETVSVIALNGRESPLILGOOSTYSDVPRDLVVAATPTSLISMDAPAVTVR 208

Db 61 LTFGTETVSVIALNGRESPLILGOOSTYSDVPRDLVVAATPTSLISMDAPAVTVR 120

QY 209 YRTTETGNSPFOEFVPGSKSTATTISGLKPGVDYTTTVAVTVGRGSPASSKPISTIN 268

Db 121 YRTTETGNSPFOEFVPGSKSTATTISGLKPGVDYTTTVAVTVGRGSPASSKPISTIN 180

QY 269 YRTTIDKPS 277

Db 181 YRTTIDTPS 189

ULT 6

basic fibroblast growth factor precursor, 22.5K form - human

N:Alternate names: bFGF; fibroblast growth factor 2; prostatic growth factor; prostatic

N:Contains: basic fibroblast growth factor, 18K form

C:Species: Homo sapiens (man)

C>Date: 31-Jul-1989 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000

C:Accession: A32398; A01537; A26842; B32878; S00297; A54316; B54316; A33624; A25824; B24

R:Prads, H.; Kaghad, M.; Prads, A.C.; Klagsbrun, M.; Lelias, J.M.; Liauzun, P.; Chalon,

Proc. Natl. Acad. Sci. U.S.A. 86, 1836-1840, 1989

A:Title: High molecular mass forms of basic fibroblast growth factor are initiated by a

A:Reference number: A32398; MUID:89184522; PMID:2538817

A:Accession: A32398

A:Molecule type: mRNA

A:Residues: 1-210 <PRA>

A:Cross-references: GB:J04513; NID:9183083; PIDN:AAA2531.1; PID:9459811

R:Shibata, F.; Baid, A.; Florjanczyk, R.Z.

Growth Factors 4, 277-287, 1991

A:Title: Functional characterization of the human basic fibroblast growth factor gene pr

A:Reference number: A61537; MUID:92110035; PMID:1764264

A:Accession: A61537

A:Molecule type: DNA

A:Residues: 1-114 <SHI>

A:Note: authors translated the codon GCA for residue 47 as Ala

R:Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.

FEBS Lett. 213, 189-194, 1987

A:Title: Cloning and expression of cDNA encoding human basic fibroblast growth factor

A:Reference number: A26642; MUID:87162468; PMID:2435575

A:Accession: A26642

A:Molecule type: mRNA

A:Residues: 56-210 <KUR>

A:Cross-references: GB:M27968; NID:9182562; PIDN:AAA2448.1; PID:9182563

R:Abraham, J.A.; Whang, J.L.; Tumbolo, A.; Merz, A.; Friedman, J.; Gospodarowicz, D.

Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986

A:Title: Human basic fibroblast growth factor: nucleotide sequence, genomic organizat

A:Reference number: A90924; MUID:87217066; PMID:3472745

A:Accession: B32878

A:Molecule type: mRNA

A:Residues: 56-210 <ABR>

A:Note: the authors translated the codon GAA for residue 108 as Gly

R:Abraham, J.A.; Whang, J.L.; Tumbolo, A.; Merz, A.; Friedman, J.; Gospodarowicz, D.

EMBO J. 5, 2523-2528, 1986

A:Title: Human basic fibroblast growth factor: nucleotide sequence and genomic organi

A:Reference number: S00297; MUID:87053817; PMID:3780670

A:Accession: S00297

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-155 <AB2>

A:Note: the authors translated the codon GAA for residue 108 as Gly

R:Shimoyama, Y.; Gotoh, M.; Ino, Y.; Sakamoto, M.; Kato, K.; Hirohashi, S.

Jpn. J. Cancer Res. 82, 1263-1270, 1991

A:Title: Characterization of high-molecular-mass forms of basic fibroblast growth fac

riogenesis.

A:Reference number: A54316; MUID:92091228; PMID:1721615

A:Accession: A54316

A:Molecule type: protein

A:Residues: 7XX, 86-88, 90-91, 93-95 <SH3>

A:Experimental source: C121 hepatocellular carcinoma cell line

A:Note: sequence extracted from NCBI backbone (NCBIF:71593) ;

A:Accession: B54316

A:Molecule type: protein

A:Residues: 7XX, 19, 21-29 <SH2>

A:Note: sequence extracted from NCBI backbone (NCBIF:71594)

R:Feige, J.D.; Bradley, J.D.; Fryburg, K.; Faris, J.; Cousins, L.C.; Barr, P.J.; Bai

J. Cell Biol. 109, 3105-3114, 1989

A:Title: Differential effects of heparin, fibronectin, and laminin on the phosphoryla

A:Reference number: A33624; MUID:90078343; PMID:2592418

A:Accession: A33624

A:Status: preliminary

A:Molecule type: protein

A:Residues: 57-210 <PRE>

R:Story, M.T.; Esch, F.; Shimasaki, S.; Sasse, J.; Jacobs, S.C.; Lawson, R.K.

Biochem. Biophys. Res. Commun. 142, 702-709, 1987

A:Title: Amino-terminal sequence of a large form of basic fibroblast growth factor is

A:Reference number: A25824; MUID:87156686; PMID:2435284

A:Accession: A25824

A:Molecule type: protein

A:Residues: 57-77 <STO>

A:Experimental source: prostate

R:Giemenes-Gallego, G.; Conn, G.; Hatcher, V.B.; Thomas, K.A.

Biochem. Biophys. Res. Commun. 135, 541-548, 1986

A:Title: Human brain-derived acidic and basic fibroblast growth factors: amino termin

A:Reference number: A90122; MUID:86186784; PMID:3964259

A:Accession: B24243

A:Molecule type: protein

A:Residues: 65-102, 104-105 <GIM>

A:Experimental source: brain

R:Gautschi, P.; Frater-Schroder, M.; Bohlen, P.

FEBS Lett. 204, 203-207, 1986

A:Title: Partial molecular characterization of endothelial cell mitogens from human b

A:Reference number: A91364; MUID:86752560; PMID:3732516

A:Accession: B24301

A:Molecule type: protein

A:Residues: 65-88, 90-98, 100 <GUV>

R:Sommer, A.; Brewer, M.T.; Thompson, R.C.; Moscatelli, D.; Presta, M.; Rifkin, D.B.

Biochem. Biophys. Res. Commun. 144, 543-550, 1987

A:Title: A form of human basic fibroblast growth factor with an extended amino termin

A:Reference number: S42242; MUID:87213238; PMID:3579930


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DB 1 PALPEGGSGAAPPFGHFKOPKRYCKNGGFFLRHPDGVGVREKSDPHIKILOAEER 60

QY 347 GYVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNYNTYRSKRYTSWYVALKR 406
DB 61 GYVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNYNTYRSKRYTSWYVALKR 120

QY 407 TGOYKLGSKRTGCGOKAI 423
DB 121 TGOYKLGSKRTGCGOKAI 137

RESULT 15
A40117
Species: Xenopus laevis (African clawed frog)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #extl_change 10-Sep-1999
C:Accession: A40117; A29618
R:Kimmelman, D.; Abraham, J.A.; Haaparanta, T.; Palisi, T.M.; Kirschner, M.W.
Science 242, 1053-1056, 1988
A:Title: The presence of fibroblast growth factor in the frog egg: its role as a natural
A:Reference number: A40117; MUID:89058621; PMID:3194757
A:Accession: A40117
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <KIM>
A:Cross-references: GB:M16067; MID:9214177; PIDN:AAA9726.1; PID:9214178; GB:M21092
R:Kimmelman, D.; Kirschner, M.
Cell 51, 869-877, 1987
A:Title: Synergistic induction of mesoderm by FGF and TGF-beta and the identification of
A:Reference number: A29618; MUID:88052890; PMID:3479265
A:Accession: A29618
A:Molecule type: mRNA
A:Residues: 95-110, 112-155 <K12>
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor

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DB 1 MAAGSITTLPALPEGGSGAAPPFGHFKOPKRYCKNGGFFLRHPDGVGVREKSDPHI 60

QY 338 KIQLOAEERGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNYNTYRSKRY 397
DB 61 KIQLOAEERGVVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNYNTYRSKRY 120

QY 398 TSWYVALKRITGOKYKLGSKRTGCGOKAIFLPMASAS 432
DB 121 TSWYVALKRITGOKYKLGSKRTGCGOKAIFLPMASAS 155
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Search completed: March 13, 2003, 09:37:11
Job time : 54 secs

RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
 RA MEDLINE-87080265; PubMed-3024962;
 RT Owens R.J., Baralle F.E.;
 RT "Mapping the collagen-binding site of human fibronectin by expression
 RT in *Escherichia coli*.";
 RL EMO J. 5:2825-2830(1986).
 RN [8]
 RP SEQUENCE OF 1441-1548.
 RA MEDLINE-82265604; PubMed-7050098;
 RT Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
 RT "The cell attachment domain of fibronectin. Determination of the
 RT primary structure.";
 RL J. Biol. Chem. 257:9593-9597(1982).
 RN [9]
 RP SEQUENCE OF 1434-1537 FROM N.A.
 RA MEDLINE-83390929; PubMed-6688418;
 RT Oldberg A., Linney E., Ruoslahti E.;
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for
 RT the cell attachment domain in human fibronectin.";
 RL J. Biol. Chem. 258:10193-10196(1983).
 RN [10]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RA MEDLINE-86111901; PubMed-3003095;
 RT Oldberg A., Ruoslahti E.;
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment
 RT domain.";
 RL J. Biol. Chem. 261:2113-2116(1986).
 RN [11]
 RP SEQUENCE OF 1712-1739 FROM N.A.
 RA MEDLINE-87026578; PubMed-3021206;
 RT Sekiguchi K., Kios A.M., Kurachi K., Yoshitake S., Hakomori S.;
 RT "Human liver fibronectin complementary DNAs: identification of two
 RT different messenger RNAs possibly encoding the alpha and beta
 RT subunits of plasma fibronectin.";
 RL Biochemistry 25:4936-4941(1986).
 RN [12]
 RP SULFATION.
 RA MEDLINE-86042625; PubMed-2414772;
 RT Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
 RT "Tyrosine sulfation of proteins from the human hepatoma cell line
 RT HepG2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
 RN [13]
 RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
 RA MEDLINE-95081153; PubMed-798369;
 RT Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
 RT "Further characterization of the NH2-terminal fibrin-binding site on
 RT fibronectin.";
 RL J. Biol. Chem. 269:31938-31945(1994).
 RN [14]
 RP STRUCTURE BY NMR OF 32-92.
 RA MEDLINE-96069779; PubMed-7583666;
 RT Potts J.R., Phan I., Williams M.J., Campbell I.D.;
 RT "High-resolution structural studies of the factor XIIIa crosslinking
 RT site and the first type 1 module of fibronectin.";
 RL Nat. Struct. Biol. 2:946-950(1995).
 RN [15]
 RP STRUCTURE BY NMR OF 182-275.
 RA MEDLINE-94141923; PubMed-8308892;
 RT Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
 RT Campbell I.D.;
 RT "Solution structure of a pair of fibronectin type 1 modules with
 RT fibrin binding activity.";
 RL J. Mol. Biol. 235:1302-1311(1994).
 RN [16]
 RP STRUCTURE BY NMR OF 406-464.
 RA MEDLINE-96179558; PubMed-9514732;
 RT Sligh H., Pickford A.R., Potts J.R., Campbell I.D.;
 RT "Solution structure of the glycosylated second type 2 module of
 RT fibronectin.";
 RL J. Mol. Biol. 276:177-187(1998).
 RN [17]
 RP STRUCTURE BY NMR OF 1447-1540.

RX MEDLINE-93046665; PubMed-1423622;
 RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
 RT "The three-dimensional structure of the tenth type III module of
 RT fibronectin: an insight into RGD-mediated interactions.";
 RL Cell 71:671-678(1992).
 RN [18]
 RP STRUCTURE BY NMR OF 1447-1540.
 RA MEDLINE-92162710; PubMed-1311202;
 RT Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,
 RT Campbell I.D.;
 RT "III module of fibronectin and secondary structure of the cell adhesion type
 RT III module of fibronectin.";
 RL Biochemistry 31:2068-2073(1992).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1535.
 RA MEDLINE-94166075; PubMed-8120888;
 RT Dickinson C.D., Veerapandian B., Dai X.-P., Hamlin R.C., Xuong N.-H.,
 RT Ruoslahti E., Ely K.R.;
 RT "Crystal structure of the tenth type III cell adhesion module of
 RT human fibronectin.";
 RL J. Mol. Biol. 236:1079-1092(1994).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1721-1991.
 RA MEDLINE-99177162; PubMed-10075919;
 RT Sharma A., Askari J.A., Humphries M.J., Jones E.Y., Stuart D.I.;
 RT "Crystal structure of a heparin- and integrin-binding segment of human
 RT fibronectin.";
 RL EMO J. 18:1468-1479(1999).
 RN [21]
 RP FUNCTION: FIBRONECTIN BINDS CELL SURFACES AND VARIOUS COMPOUNDS
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTIN
 CC IS INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC -1 SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
 CC TO A LESSER EXTENT HOMODIMERS.
 CC -1 ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" AND THE CONNECTING
 CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
 CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: PLASMA FN (SOLUBLE ALTERNATIVE FORM) IS SECRETED
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
 CC -1 PTM: SULFATED.
 CC -1 SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
 CC -1 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
 CC -1 SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III DOMAINS.
 CC -----
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 DR EMBL: M15801; AAA53376.1; -
 DR EMBL: X02761; CAA26536.1; -
 DR EMBL: M10905; AAA52462.1; -
 DR EMBL: M12549; AAA58483.1; -
 DR EMBL: M14059; AAA52463.1; -
 DR PIR: A26460; FNH0.
 DR PDB: 1TF7; 31-JAN-94.
 DR PDB: 1TTG; 31-JAN-94.
 DR PDB: 1FNA; 30-APR-94.
 DR PDB: 1FNF; 29-JAN-96.
 DR PDB: 1FBR; 15-OCT-95.
 DR PDB: 1FNH; 16-MAR-99.
 DR PDB: 2FN2; 16-SEP-98.
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 DR GeneW: HGNC:3778; FN1.
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 DR InterPro: IPR000561; EGF-like.
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Query Match 61.5%; Score 1474; DB 1; Length 2386;
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OY 241 PVDVDTITVYATGAGDSASSKPSISINRTFLDKPS-----M 278
DB 1510 PVDVDTITVYATGAGDSASSKPSISINRTFLDKPSQMOWTVDOVNSISVKMLPSSSEV 1569
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OY 310 YKNGG-----FELRH-----PDGRV 326
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OY 373 -----CVTDEC-----FFERLESNNVNTYRS-----R 395
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RESULT 2
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DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibronectin (FN).
GN FN1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Soltrop-Jensens L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
RT of internal homology.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
RT fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -!- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTEND HOMODIMERS.
CC -!- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES, CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS) MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -!- PTM: SULFATED (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -!- SIMILARITY: CONTAINS 15 FIBRONECTIN TYPE III DOMAINS.
CC -----
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CC -----
CC EMBL; K00800; AAA30521.2; -
CC PIR; A26452; FNBO.
CC HSSP; P02751; 2FN2.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR003961; FN_IIT.
CC InterPro: IPR000562; FN_Type_II.
CC InterPro: IPR000083; Fibnrcn1.
CC InterPro: IPR003962; FnIII_repeat.
CC Pfam; PF00039; fn1; 12.
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CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS00023; FIBRONECTIN_2; 2.
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CC Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
CC Sulfation; Cell adhesion; Repeat; Alternative splicing;
CC MOD_RES 1 241
CC FT 21 241
CC DOMAIN 277 577
CC COLLAGEN-BINDING.

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| FT | DOMAIN | 2217 | 2215 | FIBRONECTIN TYPE-1 49 |
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| FT | DOMAIN | 2220 | 2215 | FIBRONECTIN TYPE-1 52 |
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| FT | DOMAIN | 2225 | 2215 | FIBRONECTIN TYPE-1 57 |
| FT | DOMAIN | 2226 | 2215 | FIBRONECTIN TYPE-1 58 |
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| FT | DOMAIN | 2231 | 2215 | FIBRONECTIN TYPE-1 63 |
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| FT | DOMAIN | 2236 | 2215 | FIBRONECTIN TYPE-1 68 |
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| FT | DOMAIN | 2243 | 2215 | FIBRONECTIN TYPE-1 75 |
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| FT | DOMAIN | 2251 | 2215 | FIBRONECTIN TYPE-1 83 |
| FT | DOMAIN | 2252 | 2215 | FIBRONECTIN TYPE-1 84 |
| FT | DOMAIN | 2253 | 2215 | FIBRONECTIN TYPE-1 85 |
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| FT | DOMAIN | 2304 | 2215 | FIBRONECTIN TYPE-1 136 |
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| FT | DOMAIN | 2307 | 2215 | FIBRONECTIN TYPE-1 139 |
| FT | DOMAIN | 2308 | 2215 | FIBRONECTIN TYPE-1 140 |
| FT | DOMAIN | 2309 | 2215 | FIBRONECTIN TYPE-1 141 |
| FT | DOMAIN | 2310 | 2215 | FIBRONECTIN TYPE-1 142 |
| FT | DOMAIN | 2311 | 2215 | FIBRONECTIN TYPE-1 143 |
| FT | DOMAIN | 2312 | 2215 | FIBRONECTIN TYPE-1 144 |
| FT | DOMAIN | 2313 | 2215 | FIBRONECTIN TYPE-1 145 |
| FT | DOMAIN | 2314 | 2215 | FIBRONECTIN TYPE-1 146 |
| FT | DOMAIN | 2315 | 2215 | FIBRONECTIN TYPE-1 147 |
| FT | DOMAIN | 2316 | 2215 | FIBRONECTIN TYPE-1 148 |
| FT | DOMAIN | 2317 | 2215 | FIBRONECTIN TYPE-1 149 |
| FT | DOMAIN | 2318 | 2215 | FIBRONECTIN TYPE-1 150 |
| FT | DOMAIN | 2319 | 2215 | FIBRONECTIN TYPE-1 151 |
| FT | DOMAIN | 2320 | 2215 | FIBRONECTIN TYPE-1 152 |
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| FT | DOMAIN | 2322 | 2215 | FIBRONECTIN TYPE-1 154 |
| FT | DOMAIN | 2323 | 2215 | FIBRONECTIN TYPE-1 155 |
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| FT | DOMAIN | 2327 | 2215 | FIBRONECTIN TYPE-1 159 |
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| FT | DOMAIN | 2377 | 2215 | FIBRONECTIN TYPE-1 209 |
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| FT | DOMAIN | 2379 | 2215 | FIBRONECTIN TYPE-1 211 |
| FT | DOMAIN | 2380 | 2215 | FIBRONECTIN TYPE-1 212 |
| FT | DOMAIN | 2381 | 2215 | FIBRONECTIN TYPE-1 213 |
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| FT | DOMAIN | 2383 | 2215 | FIBRONECTIN TYPE-1 215 |
| FT | DOMAIN | 2384 | 2215 | FIBRONECTIN TYPE-1 216 |
| FT | DOMAIN | 2385 | 2215 | |

[illegible]

RP SEQUENCE FROM N.A.
RC STRAIN-Fischer; TISSUE=Liver;
RX MEDLINE=88054951; PubMed=2445560;
RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
RT "Multiple sites of alternative splicing of the rat fibronectin gene transcript.";
RL EMBL J. 6:2573-2580(1987).
RN [2]
RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
RC STRAIN-Fischer; TISSUE=Liver;
RX MEDLINE=88054950; PubMed=3119323;
RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;
RT "Organization of the fibronectin gene provides evidence for exon shuffling during evolution.";
RL EMBL J. 6:2565-2572(1987).
RN [3]
RX SEQUENCE OF 1586-2477 FROM N.A.
RA MEDLINE=84082067; PubMed=6317187;
RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;
RT "Three different fibronectin mRNAs arise by alternative splicing within the coding region.";
RL Cell 35:421-431(1983).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN OTHERS. THESE DIFFERENT PRODUCTS ARE DUE TO ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED BY HEPATOCTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE II DOMAINS.
CC -1- SIMILARITY: CONTAINS 17 FIBRONECTIN TYPE III DOMAINS.
CC -----
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CC -----
DR EMBL; X15906; CAA34020.1; -;
DR EMBL; L29191; AAA41166.1; -;
DR EMBL; L29191; AAA41166.1; JOINED.
DR EMBL; L29191; AAA41167.1; -;
DR EMBL; L29191; AAA41167.1; JOINED.
DR EMBL; L29191; AAA41168.1; -;
DR EMBL; L29191; AAA41168.1; JOINED.
DR EMBL; X05831; CAA29278.1; -;
DR EMBL; X05831; CAA29278.1; -;
DR EMBL; X05833; CAA29280.1; -;
DR EMBL; X05834; CAA29281.1; -;
DR PIR; A27252; A27252.
DR PIR; S00459; S00459.
DR PIR; S14428; S14428.
DR HSSP; P02751; 1E8R.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000083; FibrnctnI.
DR InterPro; IPR003962; FntIII_repeat.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PRO0012; FNTYPEI.
DR PRINTS; PRO0013; FNTYPEII.
DR PRINTS; PRO0014; FNTYPEIII.
DR PRODom; PD000895; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 15.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation; Cell adhesion; Cell adhesion; Repeat; Alternative splicing; Signal.
FT SIGNAL 1 32
FT CHAIN 33 2477
FT DOMAIN 53 273
FT DOMAIN 308 608
FT DNA_BIND 906 1171
FT DOMAIN 1357 1630
FT DOMAIN 1811 2081
FT DOMAIN 2296 2427
FT DOMAIN 51 91
FT DOMAIN 96 139
FT DOMAIN 140 183
FT DOMAIN 185 229
FT DOMAIN 230 274
FT DOMAIN 306 345
FT DOMAIN 345 404
FT DOMAIN 405 459
FT DOMAIN 468 511
FT DOMAIN 516 558
FT DOMAIN 559 602
FT DOMAIN 609 706
FT DOMAIN 707 808
FT DOMAIN 809 903
FT DOMAIN 904 994
FT DOMAIN 995 1084
FT DOMAIN 1085 1172
FT DOMAIN 1173 1264
FT DOMAIN 1265 1355
FT DOMAIN 1356 1446
FT DOMAIN 1447 1536
FT DOMAIN 1537 1630
FT DOMAIN 1631 1720
FT DOMAIN 1721 1810
FT DOMAIN 1811 1902
FT DOMAIN 1903 1991
FT DOMAIN 1992 2081
FT DOMAIN 2082 2201
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FT SITE 1614 1616
FT SITE 2181 2183
FT DISULFID 53 79
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FT DISULFID 168 180
FT DISULFID 187 216
FT DISULFID 214 226
FT DISULFID 232 261
FT DISULFID 259 271
FT DISULFID 308 335
FT DISULFID 333 342
FT DISULFID 360 386
FT DISULFID 374 401
FT DISULFID 420 446
FT DISULFID 434 461
FT DISULFID 470 498
FT DISULFID 496 508
FT DISULFID 518 545
FT DISULFID 543 555
CELL-ATTACHMENT.
HEPARIN-BINDING 2.
FIBRIN-BINDING 2.
FIBRONECTIN TYPE-1 1.
FIBRONECTIN TYPE-1 2.
FIBRONECTIN TYPE-1 3.
FIBRONECTIN TYPE-1 4.
FIBRONECTIN TYPE-1 5.
FIBRONECTIN TYPE-1 6.
FIBRONECTIN TYPE-1 1.
FIBRONECTIN TYPE-1 2.
FIBRONECTIN TYPE-1 7.
FIBRONECTIN TYPE-1 8.
FIBRONECTIN TYPE-1 9.
FIBRONECTIN TYPE-1 1.
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FIBRONECTIN TYPE-1 12.
FIBRONECTIN TYPE-1 13 (EXTRA DOMAIN 2).
FIBRONECTIN TYPE-1 14.
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FT DISULFID 561 589 BY SIMILARITY.
 FT DISULFID 587 599 BY SIMILARITY.
 FT DISULFID 2296 2325 BY SIMILARITY.
 FT DISULFID 2323 2335 BY SIMILARITY.
 FT DISULFID 2341 2368 BY SIMILARITY.
 FT DISULFID 2366 2378 BY SIMILARITY.
 FT DISULFID 2385 2409 BY SIMILARITY.
 FT DISULFID 2407 2423 BY SIMILARITY.
 FT DISULFID 2458 2458 INTERCHAIN (WITH 2462 OF OTHER CHAIN).
 FT CARBOHYD 2462 2462 INTERCHAIN (WITH 2458 OF OTHER CHAIN).
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1290 1290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2198 2198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 2475 2475 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPLIC 1720 1809 MISSING (IN ISOFORM FNII-13 LESS).
 FT VARSPLIC 2082 2106 MISSING (IN ISOFORM LAMBDA-RLF4-5).
 FT VARSPLIC 2082 2200 MISSING (IN ISOFORM LAMBDA-RLF6).
 FT CONFLICT 2318 2318 G -> A (IN REF. 3).
 SQ SEQUENCE 2477 AA; 272510 MW; B4391A472CEDEB5 CRC64;

Query Match 56.1%; Score 1345; DB 1; Length 2477;
 Best local Similarity 42.4%; Pred. No. 1.3e-88;
 Matches 318; Conservative 49; Mismatches 87; Indels 296; Gaps 18;

1 FTDLRTNIGPDIMRYTAPPSIDLTNPLVRSYKNEEDVAELSTSPDNVLTNLL 60
 1360 FTDLRTNIGPDIMRYTAPPSIDLTNPLVRSYKNEEDVAELSTSPDNVLTNLL 1419
 61 PCGEYVAVSVYEHESPTLGRKGTGDSPTGIDPSDTANSFYHMAIPATITGR 120
 1420 PCGEYVAVSVYEHESPTLGRKGTGDSPTGIDPSDTANSFYHMAIPATITGR 1479
 121 IRHHPFSGRPREDRYPHSRNSITLTNLTGEYVAVSVYALNGREBSPLLICQSTVSD 180
 1480 IRHHAHSARPRQDRVPSRNSITLTNLTGEYVAVSVYALNGREBSPLLICQSTVSD 1539
 181 VPRDLEVVATPTSLISMDAPAVYRYRTYGETGNSPVQETVPQSGSTATISGLK 240
 1540 VPRDLEVVATPTSLISMDAPAVYRYRTYGETGNSPVQETVPQSGSTATISGLK 1599
 241 PCVDYITTVAVTGRGDSPPASPKPISINYTEIDKPS-----M 278
 1600 PGADYITTVAVTGRGDSPPASPKPISINYTEIDKPSQMQVTDVODNSISVRLPSTSPV 1659
 279 AAGSITTLT----- 287
 1660 TGYRVTTAPKNGLGPTKRSQVSPDQEMTIEGLQPTVEYVSVYAQNRGESQPLVQTAV 1719
 288 -----ALPEDGSGSAFP-PGHPKPKRL 309
 1720 TNIDRPKGLAFDVDDSIKIAMESPOGVSRVRYTSSPEDIHFLFPADDEDTAEL 1779
 310 Y-----CKNGG-----FLKIH-----EDGRV 326
 1780 HGLRPGSEYVSVYALNGREBSPPLIGVOSTAIPAPNPKLTQVSPPTTLTAQMTAVSVKL 1839
 327 DGYR-----EKSDPHIKILOAEBRGVSVIKVCANRY---LAKEDRGLASK--- 372
 1840 TGYRVVTPREKTKPMKEINLSPDSTSVIVSGLMVARKVSVYALKD---TLTSRAOG 1896
 373 -----CVTDEC-----FFERLESNNY----- 389
 1897 VVTTLENVSPRRARVYDATTITTSWRTETITGFOVDALPANCQTPVORTISPDVR 1956
 390 -----NTRSRKYT-----SWYA 403
 1957 SYTITGLOPCTDYKIHLYTLINDNARSSPVYIDASTAIDAPSNLRLTTPNSLLVSNQAP 2016

OY 404 LKRTGOY-----KLGRK-----TG--PGOKAILFL-----PW- 428
 DB 2017 RARITGYIIKYEKPSPREVPVPRPGVTEATITGLERGTEYTYIVALKNOKSEPLI 2076
 OY 429 -SASDELPOVLTLPNPHGPIIDVPST 457
 DB 2077 GRKTDLPOLVTLPHPNHGPIDLPST 2106

RESULT 4

FINC_MOUSE ID FINC_MOUSE STANDARD: PRT: 2477 AA.
 AC P11276; 061568; 061569; 061567; 064233;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibronectin precursor (FN) (Fragments).
 GN FNI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE OF 1-28 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=941313; PubMed=8299972;
 RA Polly P., Nicholson R.C.;
 RT "Sequence of the mouse fibronectin-encoding gene promoter region.";
 RL Gene 137:353-354(1993).
 RN [2]
 RP SEQUENCE OF 562-834 FROM N.A.
 RC STRAIN=MRI;
 RX MEDLINE=95403556; PubMed=7673336;
 RA Tates J.F., Weller A., Timpi R., Ekblom M., Ekblom P.;
 RT Regulation of mesenchymal extracellular matrix protein synthesis by
 RT transforming growth factor-beta and glucocorticoids in tumor
 RT stroma.";
 RL J. Cell Sci. 108:2153-2162(1995).
 RN [3]
 RP SEQUENCE OF 899-2376 FROM N.A.
 RA Gorski G., Aros M., Norton P.;
 RT Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RX MEDLINE=88124987; PubMed=3124113;
 RA Blati S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;
 RT "Induction of fibronectin gene transcription and mRNA is a primary
 RT response to growth-factor stimulation of AKR-2B cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
 RN [5]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93011702; PubMed=1327855;
 RA Khadjian E.W., Salomon C., Leonard N., Tremblay S., Turlier H.;
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
 RT infected mouse kidney cells.";
 RL Exp. Cell Res. 202:464-470(1992).
 RN [6]
 RP STRUCTURE BY NMR OF 1447-1630.
 RX MEDLINE=98202578; PubMed=9533887;
 RA Cople V., Tomita Y., Akiyama S.K., Acta S., Yamada K.M., Venable R.M.,
 RA Pastor R.W., Krueger S., Torchia D.A.;
 RT "Solution structure and dynamics of linked cell attachment modules of
 RT mouse fibronectin containing the RGD and synergy regions: comparison
 RT with the human fibronectin crystal structure.";
 RL J. Mol. Biol. 277:663-682(1998).
 CC -I- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 CC HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC -I- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 CC VARIANTS. CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS.
 CC TO A LESSER EXTENT HOMODIMERS.

QY 370 ASK-----CVTDEC-----FFERLESNNY----- 389
 DB 1890 TSPRAGVITTELENSPPRRARVDTATETTTITSMRTKETITGQVDAIPANGCPVOR 1949
 QY 390 -----NRYRSRKYT----- 398
 DB 1950 SISPDVRSYITGLPGCTDYKILHVLTLNDNARNSSPYIIDASTAIDAPNSLRELTTPNSL 2009
 QY 399 --SWVVALKRTGQY-----KLGSK-----TG--PGKAILFL----- 426
 DB 2010 LVSMQAPRARTIGYIIKRYKPCSPREVPYRPRPGTEATITGLEGTETTYIYALKRN 2069
 QY 427 ----PM--SAASDELPLYTLPHPNHGPILLDPST 457
 DB 2070 OKSEPLIGKRTDELPLVTLPHPNHGPILLDPST 2106

RESULT 5

FINC_CHICK STANDARD: PRT: 1256 AA.

01-OCT-1989 (rel. 12, Created)
 01-NOV-1997 (rel. 35, Last sequence update)
 16-NOV-2001 (rel. 40, Last annotation update)
 DE Fibronectin (FN) (Fragments).
 GN FN1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 1-50 FROM N.A.
 RX MEDLINE=83117850; PubMed=6572007;
 RA Yamada K.M., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,
 RT "Isolation of genomic DNA clones spanning the entire fibronectin
 gene." Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).
 RL [2]
 RN [2]
 RP SEQUENCE OF 51-1256 FROM N.A.
 RC STRAIN=White Leghorn;
 RA Norton P.A.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 227-415 FROM N.A.
 RX MEDLINE=96183658; PubMed=8603103;
 RA Gehris A.L., Brandl D.W., Lewis S.D., Bennett V.D.;
 RT "The exon encoding the fibronectin type III-9 repeat is
 constitutively included in the mRNA from chick limb mesenchyme and
 cartilage." J. Biol. Chem. 268:13111-13115(1993).
 RL [4]
 RN [4]
 RP SEQUENCE OF 327-599 FROM N.A.
 RX MEDLINE=88050950; PubMed=2823899;
 RA Tsuda T., Higashi K., Ohsato K., Hiaro H.;
 RT "Genetic analysis of the cell binding domain region of the chicken
 fibronectin gene." Acta 910:171-181(1987).
 RL [5]
 RN [5]
 RP SEQUENCE OF 413-1256 FROM N.A.
 RX MEDLINE=88142820; PubMed=2830487;
 RA Norton P.A., Hynes R.O.;
 RT "Alternative splicing of chicken fibronectin in embryos and in normal
 and transformed cells." J. Biol. Chem. 263:14307-14311(1988).
 RL [6]
 RN [6]
 RP FUNCTION: FIBRONECTIN BIND CELL SURFACES AND VARIOUS COMPOUNDS
 INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTIN
 ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 HEALING, AND MAINTENANCE OF CELL SHAPE.
 CC - SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
 CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS.

CC TO A LESSER EXTEND HOMODIMERS.
 CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
 CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
 CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
 CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
 CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
 CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
 CC -1- PTM: SULFATED (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS AT LEAST 2 FIBRONECTIN TYPE I DOMAINS.
 CC -1- SIMILARITY: CONTAINS AT LEAST 8 FIBRONECTIN TYPE III DOMAINS.
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 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC -----
 CC EMBL: V00432; CAA23714.1;
 CC EMBL: U21327; AAA73566.1;
 CC EMBL: X06533; CAA29781.1;
 CC EMBL: M26186; AAA48772.1; ALT_SEQ.
 CC EMBL: U20386; AAB01062.1;
 CC PIR: A28512; A28512.
 CC PIR: A29355; A29355.
 CC HSSP: P02751; 1FNH.
 CC InterPro: IPR003961; FN_III.
 CC InterPro: IPR000562; FN_Type_II.
 CC InterPro: IPR000083; Fibnctnl.
 CC InterPro: IPR003962; FnIII_repeat.
 CC PRINTS: PR00014; FNTypeIII.
 CC SMART: SM00058; FN1_3.
 CC SMART: SM00060; FN3_10.
 CC PROSITE: PS00023; FIBRONECTIN_2; PARTIAL.
 CC PROSITE: PS01253; FIBRONECTIN_1; 2.
 CC Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 CC FT NON_TER 1 1
 CC FT 50 51
 CC FT 236 509
 CC FT 690 961
 CC FT 1153 1226
 CC FT 327 415
 CC FT 416 509
 CC FT 510 689
 CC FT 600 781
 CC FT 782 871
 CC FT 872 961
 CC FT 962 1082
 CC FT 1083 1152
 CC FT 1174 1218
 CC FT 1219 1256
 CC FT 483 485
 CC FT 1176 1205
 CC FT DISULFID 1203 1245
 CC FT DISULFID 1221 1248
 CC FT CARBOHYD 1078 1078
 CC FT CONFLICT 516 516
 CC FT CONFLICT 569 572
 CC FT NON_TER 1256 1256
 CC SQ SEQUENCE 1256 AA; 137435 MW; 345A4CA0E471D9B CRC64;
 Query Match 50.5%; Score 1210.5; DB 1; Length 1256;
 Best Local Similarity 76.3%; Pred. No. 2.5e-79;
 Matches 238; Conservative 23; Mismatches 32; Indels 19; Gaps 2;
 QY 1 PDLARTNIGPDMRTWMPSPSIDLNFVRSVPKNEDEVAELSTSPDNAAVLTNLL 60
 DB 239 PDLARTNIGPDMRTWMPSPSIDLNFVRSVPKNEDEVAELSTSPDNAAVLTNLL 298

| CC | Accession | Protein Name | Gene Name | Species | Length (aa) | Weight (kDa) | PI | CD |
|----|-------------------------------------|--|-----------|---------|-------------|--------------|-----|----|
| DR | EMBL: X66813; CAA47292.1; . | InterPro: IPR000561; EGF-like. | EGF | Human | 121 | 13.5 | 5.5 | 1 |
| DR | HSSP: P02751; 1FNH. | InterPro: IPR003961; FN_III. | FN3 | Human | 107 | 12.5 | 5.5 | 1 |
| DR | InterPro: IPR000083; Fibrinctn1. | Pfam: PF000039; fn1; 3. | FBN1 | Human | 2454 | 275 | 5.5 | 1 |
| DR | Pfam: PF000041; fn3; 11. | SMART: SM00058; FN1; 3. | FBN1 | Human | 2454 | 275 | 5.5 | 1 |
| DR | SMART: SM00060; FN3; 9. | PROSITE: PS00022; EGF_1; 1. | EGF | Human | 121 | 13.5 | 5.5 | 1 |
| DR | PROSITE: PS01253; FIBRONECTIN_1; 1. | Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion; | FBN1 | Human | 2454 | 275 | 5.5 | 1 |
| KW | Repeat. | | | | | | | 1 |
| KW | NON_TER | | | | | | | 1 |

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|----|-----|--|-----|
| QY | 2 | TDLFFNTNGPDTMKTWAPRPSIDLTJLFLVYSPKNEEDVAELISPSDNAAVLTLPLP | 61 |
| QY | | | |
| Db | 207 | TLDRFTNGGPDMSMLVTWAPSAPMSLFLVRYVPSKNEEDAAELTILISPDNMVVLTLPLP | 266 |
| QY | 62 | GTEVYVSSSVYEOHESPRLRGROKTGLDSTGIDSESDITANSTYVWIAVPRATTCYRI | 121 |
| QY | | | |
| Db | 267 | GTEIVASFPAYIEEESRPLTGLGVORTGLDSTGLDSESDITSSSTFYVWMAVPRATVGYKI | 326 |
| QY | 122 | RHHDEHFSGRPREDR-VPHSNSTLTTLNLPLPGTEVYVSVIALNLRGEESPPLLIQOQSTVD | 180 |
| QY | | | |
| Db | 327 | QYHDETGCAGCKEERCVPYPSKNSLTTLNLPGTEVYVSVIAVNGROESVLYCOQATVSD | 386 |
| QY | 181 | VERDLEVAAPRTSLTSLTSMWDPAATVYVYRTYTGEGTGNSPVOEFTYPPGSKVATISGLK | 240 |
| QY | | | |
| Db | 387 | TFTNLEAVTSSFTPMISLMSWDAPRYGVYKRYRTTYETTGEGTFRPYOEFYTPGRSDAPIRGLK | 446 |
| QY | 241 | PGVDYTTITVAVATRGDSDPASKRISTINRYETDKPS | 277 |
| QY | | | |
| Db | 447 | PGAEEIITVAVATRGDSDPASKRISTVYTHKIKVVDKPT | 483 |

| RESULT 7 | FINC_XENLA | STANDARD | PRT: 2481 AA. |
|------------|---|----------|---------------|
| ID | FINC_XENLA | | |
| AC | 091740: | | |
| DT | 01-NOV-1997 (Rel. 35, Created) | | |
| DT | 01-NOV-1997 (Rel. 35, Last sequence update) | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | |
| DE | Fibrinectin precursor. | | |
| GN | FN1. | | |
| OS | <i>Xenopus laevis</i> (African clawed frog). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; | | |
| OC | Xenopodinae; Xenopus. | | |
| NCBI_TaxID | 8355; | | |

[1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92111942; PubMed=1730390;
 RA Desimone D.W., Norton P.A., Hynes R.O.;
 RT "Identification and characterization of alternatively spliced
 RT fibronectin mRNAs expressed in early Xenopus embryos.";
 RT Dev. Biol. 149:357-369(1992).
 CC -1- FUNCTION: FIBRONECTIN BIND CELL SURFACES AND VARIOUS COMPOUNDS
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 CC HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).
 CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
 CC CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
 CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
 CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
 CC FIBRONECTIN PREDOMINATE WHICH INCLUDE BOTH EXTRA DOMAINS. IN
 CC FIBRONECTIN FROM EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
 CC CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
 CC -1- SIMILARITY: CONTAINS 12 FIBRONECTIN TYPE I DOMAINS.
 CC -1- SIMILARITY: CONTAINS 17 FIBRONECTIN TYPE III DOMAINS.
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 CC -----
 DR EMBL: M77820; AAA49707.1; .
 DR HSSP: P02751; 2FN2.
 DR InterPro: IPR0000561; EGF-like.
 DR InterPro: IPR0003961; FN_III.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000083; Fibrctn1.
 DR InterPro: IPR003962; FNIII_repeat.
 DR Pfam: PF000039; fn1; 12.
 DR Pfam: PF000040; fn2; 2.
 DR Pfam: PF000041; fn3; 17.
 DR PRINTS: PR00012; FNYPE1.
 DR PRINTS: PR00013; FNYPE1.
 DR PRINTS: PR00014; FNYPE1II.
 DR ProDom: PD000995; FN_Type_II; 2.
 DR SMART: SM00058; FN1; 12.
 DR SMART: SM00059; FN2; 2.
 DR SMART: SM00060; FN3; 17.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS01253; FIBRONECTIN_1; 11.
 DR GlycoProtein: Plasma; Heparin-binding; Acute phase; Cell adhesion;
 DR Repeat: Alternative splicing; Signal.
 KW SIGNAL 31
 FT CHAIN 32 2481
 FT DOMAIN 55 275
 FT DNA_BIND 309 609
 FT DOMAIN 907 1172
 FT DOMAIN 1358 1631
 FT DOMAIN 1812 2082
 FT DOMAIN 2301 2432
 FT DOMAIN 53 93
 FT DOMAIN 98 141
 FT DOMAIN 142 185
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 FT DOMAIN 307 346
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 DB 1481 IRKQLESGAGRKEERVPSPRSNITLTHLPGEYVYSIVALNGQOESLPLAQOQAVSD 1540
 OY 181 VPRDLEVPATPTSLTISMDAPAVYRYRYTGTGNSPVOEFTVPGSKSTATISGLK 240
 DB 1541 VPFDLEVTSSPMTLTISMEAPAVSYRYRYTSQTGHPGEKEFVTPGTSNATIRGLN 1600
 OY 241 PGVDYTIIVYATYGRGDSRASSKPISTINRTEIDKP-SNAAGSI 283
 DB 1601 PGVSYTIIVYAVYGRGDSRASSKPLTIHKTVDQPIDMAVTDI 1644
 RESULT 8
 FGF2_HUMAN
 ID FGF2_HUMAN STANDARD: PRT: 155 AA.
 AC P09038;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatopin).
 GN FGF2 OR FGFb.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Friedman J., Gospodarowicz D., Fiddes J.C.;
 RT "Human basic fibroblast growth factor: nucleotide sequence and genomic organization.";
 RL EMBO J. 5:2523-2528(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;
 RT "Human basic fibroblast growth factor: nucleotide sequence, genomic organization, and expression in mammalian cells.";
 RL Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sommer A., Brewer M.T., Thompson R.C., Moscatelli D., Presta M., Rifkin D.B.;
 RT "A form of human basic fibroblast growth factor with an extended amino terminus.";
 RL Biochem. Biophys. Res. Commun. 144:543-550(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Kurukawa T., Sasada R., Iwane M., Igarashi K.;
 RT "Cloning and expression of cDNA encoding human basic fibroblast growth factor.";
 RL FEBS Lett. 213:189-194(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-89184522; PubMed-2538817;
 RA Prats H., Kaghad M., Prats A.C., Klagsbrun M., Lelias J.M., Lianzun P., Chalon P., Tauber J.P., Amalric F., Smith J.A., Caput D.;
 RT "High molecular mass forms of basic fibroblast growth factor are initiated by alternative CUG codons.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1836-1840(1989).
 RN [6]
 RP SEQUENCE OF 10-35.
 RA MEDLINE-86275260; PubMed-3732516;
 RA Gauschl P., Frater-Schroeder M., Boehlen P.;
 RT "Partial molecular characterization of endothelial cell mitogens from human brain: acidic and basic fibroblast growth factors.";

RL FEBS Lett. 204:203-207(1986).
 RN [7]
 RP SEQUENCE OF 10-39.
 RX MEDLINE-86186784; PubMed-3964259;
 RA Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
 RT "Human brain-derived acidic and basic fibroblast growth factors: amino terminal sequences and specific mitogenic activities.";
 RL Biochem. Biophys. Res. Commun. 135:541-548(1986).
 RN [8]
 RP SEQUENCE OF 2-22.
 RX MEDLINE-87156686; PubMed-2435284;
 RA Story M.T., Esch F., Shinasaki S., Sasse J., Jacobs S.C., Lawson R.K.;
 RT "Amino-terminal sequence of a large form of basic fibroblast growth factor isolated from human benign prostatic hyperplastic tissue.";
 RL Biochem. Biophys. Res. Commun. 142:702-709(1987).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-91195367; PubMed-1707542;
 RA Eriksson A.E., Cousens L.S., Weaver L.H., Matthews B.W.;
 RT "Three-dimensional structure of human basic fibroblast growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3441-3445(1991).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE-94004464; PubMed-7691311;
 RA Eriksson A.E., Cousens L.S., Matthews B.W.;
 RT "Refinement of the structure of human basic fibroblast growth factor at 1.6-A resolution and analysis of presumed heparin binding sites by selenate substitution.";
 RL Protein Sci. 2:1274-1284(1993).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE-91195368; PubMed-1849658;
 RA Zhang J., Cousens L.S., Barr P.J., Sprang S.R.;
 RT "Three-dimensional structure of human basic fibroblast growth factor, a structural homolog of interleukin 1 beta.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3446-3451(1991).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE-92121151; PubMed-1769963;
 RA Ago H., Kitegawa Y., Fujishima A., Matsuura Y., Katsube Y.;
 RT "Crystal structure of basic fibroblast growth factor at 1.6-A resolution.";
 RL J. Biochem. 110:360-363(1991).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE-91095983; PubMed-1702556;
 RA Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T., Hsu B.T., Rees D.C.;
 RT "Three-dimensional structures of acidic and basic fibroblast growth factors.";
 RL Science 251:90-93(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97040521; PubMed-8885834;
 RA Moy F.J., Seddon A.P., Boehlen P., Powers R.;
 RT "High-resolution solution structure of basic fibroblast growth factor determined by multidimensional heteronuclear magnetic resonance spectroscopy.";
 RL Biochemistry 35:13552-13561(1996).
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC *****
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 CC -----
 DR EMBL: M17599: AAA52534.1: ALT_INIT.
 DR EMBL: X04431: CAA28027.1: -
 DR EMBL: X04432: CAA28028.1: -
 DR EMBL: X04433: CAA28029.1: -
 DR EMBL: M27658: AAA52448.1: -
 DR EMBL: J04513: AAA52553.1: ALT_INIT.
 DR PIR: A26824: A26824.
 DR PIR: A26842: A26842.
 DR PIR: B24243: B24243.
 DR PIR: B24301: B24301.
 DR PIR: B32878: B32878.
 DR PIR: S00297: S00297.
 DR PDB: 2EGF: 15-APR-92.
 DR PDB: 4EGF: 15-JUL-93.
 DR PDB: 1FGA: 15-JUL-93.
 DR PDB: 1BFB: 03-APR-96.
 DR PDB: 1BFC: 03-APR-96.
 DR PDB: 1BFF: 16-JUN-97.
 DR PDB: 1BFG: 31-JAN-94.
 DR PDB: 2BFG: 30-APR-94.
 DR PDB: 1BLA: 08-NOV-96.
 DR PDB: 1BLD: 08-NOV-96.
 DR Gene: HGNC:3676; FGF2.
 DR MIM: 134920: -
 DR InterPro: IPR002309; HB/F_growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HBGF.
 DR PRODOM: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; EGF; 1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding;
 DR 3d-structure.
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 Best Local Similarity 99.48; Pred. No. 1.8e-52;

Matches 154; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 MAAGSTITLPALEPDGSGAPPGHFKDPKRLCYCKNGGFELRHDPGRVDGVRKSDPHI 60
 OY 338 KIQLQAEERGVYSIKVCANRYLAMKEDGRLLASKVYTBCEFFELSENNTYRSKY 397
 DB 61 KIQLQAEERGVYSIKVCANRYLAMKEDGRLLASKVYTBCEFFELSENNTYRSKY 120
 OY 398 TSWYVALKRTGQYKLGSKTGPGOKAILFLPMSAAS 432
 DB 121 TSWYVALKRTGQYKLGSKTGPGOKAILFLPMSAAS 155
 RESULT 9
 FGF2_BOVIN STANDARD; PRT; 155 AA.
 ID FGF2_BOVIN STANDARD; PRT; 155 AA.
 AC P03969;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast
 DE growth factor) (BGF) (Prostatropin) [Contains: Kidney-derived growth
 DE factor].
 GN FGF2 OR FGF-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86261806; PubMed-2425435;
 RA Abraham J.A., Mergia A., Whang J.L., Tumolo A., Friedland J.,
 RA Hjerild K.A., Gospodarowicz D., Fiddes J.C.;
 RT Nucleotide sequence of a bovine clone encoding the angiogenic
 RT protein, basic fibroblast growth factor.";
 RL Science 233:545-548(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87217066; PubMed-3472745;
 RA Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;
 RT Human basic fibroblast growth factor: nucleotide sequence, genomic
 RT organization, and expression in mammalian cells.";
 RL Cold Spring Harb. Symp. Quant. Biol. 51:657-668(1986).
 RN [3]
 RP SEQUENCE OF 10-155.
 RX MEDLINE-86016731; PubMed-3863109;
 RA Esch F., Baird A., Ling N., Ueno N., Hill F., Denoroy L., Klepper R.,
 RA Gospodarowicz D., Boehlen P., Guillemin R.;
 RT Primary structure of bovine pituitary basic fibroblast growth factor
 RT (FGF) and comparison with the amino-terminal sequence of bovine brain
 RT acidic FGF.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6507-6511(1985).
 RN [4]
 RP SEQUENCE OF 1-9.
 RX MEDLINE-86295737; PubMed-3741423;
 RA Ueno N., Baird A., Esch F., Ling N., Guillemin R.;
 RT "Isolation of an amino terminal extended form of basic fibroblast
 RT growth factor.";
 RL Biochem. Biophys. Res. Commun. 138:580-588(1986).
 RN [5]
 RP SEQUENCE OF 25-41.
 RC TISSUE=Kidney;
 RX MEDLINE-86095426; PubMed-4081126;
 RA Baird A., Esch F., Boehlen P., Ling N., Gospodarowicz D.;
 RT "Isolation and partial characterization of an endothelial cell growth
 RT factor from the bovine kidney: homology with basic fibroblast growth
 RT factor.";
 RL Regul. Pept. 12:201-213(1985).
 RN [6]
 RP SEQUENCE OF 21-40.

RC TISSUE=Kidney;
 RX MEDLINE=87119165; PubMed=3809608;
 RA Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Gullermin R.;
 RT "Purification and partial characterization of a mitogenic factor from
 RT bovine liver: structural homology with basic fibroblast growth
 RT factor.";
 RL Regul. Pept. 16:135-145(1986).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA MEDLINE=91095983; PubMed=1702556;
 RA Zhu X., Komiyama H., Chirino A., Faham S., Fox G.M., Arakawa T.,
 RA Hsu B.T., Rees D.C.;
 RT "Three-dimensional structures of acidic and basic fibroblast growth
 RT factors.";
 RL Science 251:90-93(1991).
 CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
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 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES
 CC AEGF.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC -----
 DR EMBL: M13440; AAA30518.1; -
 DR PIR: A24663; GKBOB.
 DR PIR: A24819; A24819.
 DR PIR: A32878; A32878.
 DR PDB: 1BAS; 31-OCT-93.
 DR InterPro: IPR002209; HB/F_growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; FGF; 1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF; 1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding;
 KW 3D-structure.
 KM
 FT PROPEP 1 9
 FT CHAIN 10 155 HEPARIN-BINDING GROWTH FACTOR 2.
 FT SITE 25 155 KIDNEY-DERIVED GROWTH FACTOR.
 FT SITE 46 48 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 88 90 CELL ATTACHMENT SITE (POTENTIAL).
 FT BINDING 27 31 HEPARIN (POTENTIAL).
 FT BINDING 116 119 HEPARIN (POTENTIAL).
 FT BINDING 30 34
 FT TURN 35 38
 FT STRAND 39 43
 FT STRAND 45 46
 FT STRAND 49 52
 FT STRAND 55 56
 FT STRAND 58 60
 FT STRAND 62 68
 FT STRAND 69 70
 FT STRAND 71 76
 FT STRAND 77 80
 FT STRAND 81 85
 FT STRAND 87 88
 FT STRAND 91 94
 FT HELIX 99 101
 FT STRAND 103 107
 FT TURN 109 110
 FT STRAND 113 117
 FT TURN 121 122
 FT STRAND 124 124

FT STRAND 127 127
 FT TURN 129 130
 FT STRAND 133 133
 FT HELIX 136 138
 FT TURN 141 142
 FT HELIX 144 146
 FT STRAND 148 151
 SQ SEQUENCE 155 AA; 17250 MW; BEGCE70FA6107129 CRC64;
 Query Match 33.8%; Score 811; DB 1; Length 155;
 Best Local Similarity 98.1%; Pred. No. 8e-52;
 Matches 152; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 278 MANGSTTLPALPEDGSGAFPFGHFKDPRLCKNGGFEFLRHPDGRVGVREKSDPHI 337
 DB 1 MANGSTTLPALPEDGSGAFPFGHFKDPRLCKNGGFEFLRHPDGRVGVREKSDPHI 60
 QY 338 KLOLAEBRGVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNYTSRKY 397
 DB 61 KLOLAEBRGVSIKVCANRYLAMKEDGRLASKCVTDECFEERLESNNYTSRKY 120
 QY 398 TSNVVALKRTGYKLGSKTGPQKAILFLPMSAAS 432
 DB 121 SSVYVALKRTGYKLGKTPGQKAILFLPMSAKS 155
 RESULT 10
 FGF2_SHEEP
 ID FGF2_SHEEP STANDARD; PRT; 155 AA.
 AC P20003;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast
 DE growth factor) (BFGF) (Prostatropin).
 GN FGF2 OR FGF-2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 9-155.
 RX MEDLINE=88055577; PubMed=3678486;
 RA Simpson R.J., Moritz R.L., Lloyd C.J., Fabri L.J., Nice E.C.,
 RA Rubira M.R., Burgess A.W.;
 RT "Primary structure of ovine pituitary basic fibroblast growth
 RT factor.";
 RL FEBS Lett. 224:128-132(1987).
 CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES
 CC AEGF.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L36136; AAA31519.1; -
 DR PIR: S00185; S00185.
 DR HSSP: P09038; 1BFF.

DR InterPro: IPR002209; HB/F-growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; FGF; 1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F-growthfact; 1.
 DR SMART: SM00442; FGF; 1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding.
 FT CHAIN 1 155
 FT SITE 45 48 HEPARIN-BINDING GROWTH FACTOR 2.
 FT SITE 87 90 CELL ATTACHMENT SITE (POTENTIAL).
 FT BINDING 27 31 CELL ATTACHMENT SITE (POTENTIAL).
 FT BINDING 116 119 HEPARIN (POTENTIAL).
 SQ SEQUENCE 155 AA: 17280 MW: 35723646 Da B610606D CRC64;

Query Match 33.6%; Score 805; DB 1; Length 155;
 Best Local Similarity 97.4%; Pred. No. 2.2e-51;
 Matches 151; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

278 MAGSTITLPLALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVRKSDPHI 337
 1 MAAGSTITLPLALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVRKSDPHI 60
 338 KQLQAEERGVSVIKGCANRYLAMKEDGRLLASCKVTECEFFERLESNNYNTYRSRY 397
 61 KQLQAEERGVSVIKGCANRYLAMKEDGRLLASCKVTECEFFERLESNNYNTYRSRY 120
 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
 121 SSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 155

RESULT 11
 FGF2_RAT STANDARD: PRT; 154 AA.

AC P13109;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (prolactropin).
 GN FGF2 OR FGF-2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;
 RN SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=89061721; PubMed=3196337;
 RA Shimazaki S., Emoto N., Koba A., Mercado M., Shibata F.,
 RA Cooksey K., Baird A., Ling N.,
 RT "Complementary DNA cloning and sequencing of rat ovarian basic fibroblast growth factor and tissue distribution study of its mRNA."
 RL Biochem. Biophys. Res. Commun. 157:256-263(1988).
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88262516; PubMed=3387229;
 RA Kurokawa T., Seno M., Igarashi K.,
 RT "Nucleotide sequence of rat basic fibroblast growth factor cDNA."
 RL Nucleic Acids Res. 16:5201-5201(1988).
 RN SEQUENCE OF 1-28 FROM N.A.
 RP STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=97200905; PubMed=9048734;
 RA Pasumathil K.B.S., Jin Y., Cattini P.A.,
 RT "Cloning of the rat fibroblast growth factor-2 promoter region and its response to mitogenic stimuli in glioma C6 cells."
 RL J Neurochem. 68:898-908(1997).
 RN SEQUENCE OF 35-154 FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=92329546; PubMed=1378302;
 RA El-Husseini A.E.-D., Paterson J.A., Myal Y., Shiu R.P.C.,
 RT "PCR detection of the rat brain basic fibroblast growth factor (bFGF) mRNA containing a unique 3' untranslated region."
 RL Biochem. Biophys. Acta 1131:314-316(1992).
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1- SUBUNIT MONOMER.
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES EXAMINED.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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DR EMBL: M22427; AAA1210.1; -
 DR EMBL: X07285; CAA30265.1; -
 DR EMBL: U78079; AAC53225.1; -
 DR EMBL: X61697; CAA3863.1; -
 DR PIR: S00876; S00876.
 DR PIR: A31674; A31674.
 DR HSSP: P09038; 1BFF.
 DR InterPro: IPR002209; HB/F-growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; FGF; 1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F-growthfact; 1.
 DR SMART: SM00442; FGF; 1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
 FT PROPEP 1 9
 FT CHAIN 10 154 HEPARIN-BINDING GROWTH FACTOR 2.
 FT BINDING 26 30 HEPARIN (POTENTIAL).
 FT BINDING 115 118 HEPARIN (POTENTIAL).
 SQ SEQUENCE 154 AA: 17139 MW: 14081464 Da 23D6403 CRC64;

Query Match 33.0%; Score 792.5; DB 1; Length 154;
 Best Local Similarity 96.1%; Pred. No. 1.7e-50;
 Matches 149; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 278 MAGSTITLPLALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVRKSDPHI 337
 DB 1 MAAGSTITLPLALPEDGSGAPPGHFKDPKRLCKNGGFLRIHPDGRVDGVRKSDPHI 59
 QY 338 KQLQAEERGVSVIKGCANRYLAMKEDGRLLASCKVTECEFFERLESNNYNTYRSRY 397
 DB 60 KQLQAEERGVSVIKGCANRYLAMKEDGRLLASCKVTECEFFERLESNNYNTYRSRY 119

QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
 DB 120 SSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 154

RESULT 12
 FGF2_MOUSE STANDARD: PRT; 154 AA.
 AC P15655;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (prolactropin).
 GN FGF2 OR FGF-2.
 OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RN MEDLINE=90201563; PubMed=2318343;
 RX Hebert J.M., Basilio C., Goldfarb M., Haub O., Martin G.R.;
 RT "Isolation of cDNAs encoding four mouse EGF family members and
 RT characterization of their expression patterns during embryogenesis.";
 RL Dev. Biol. 138:454-463(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, A/J, and MOD/LtJ; TISSUE=Spleen;
 RA Ma R.Z., Teuscher C.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES
 CC AFGF.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M30644; AAC37621.1; -
 DR EMBL: AF065903; AAC17503.1; -
 DR EMBL: AF065904; AAC17504.1; -
 DR EMBL: AF065905; AAC17505.1; -
 DR PIR: C37360; C37360.
 DR HSSP: P09038; 1BPF.
 DR MGI: 95516; Fgf2.
 DR InterPro: IPR002209; HB/F_growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HBGF_FGF_1.
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding.
 KW PROPEP 1 9
 FT CHAIN 1 154 HEPARIN-BINDING GROWTH FACTOR 2.
 FT BINDING 26 30 HEPARIN (POTENTIAL).
 FT BINDING 115 118 HEPARIN (POTENTIAL).
 FT BINDING 154 AA: 17153 MW: 689677416274388 CRC64;
 SQ SEQUENCE

Query Match 32.4%; Score 777.5; DB 1; Length 154;
 Best Local Similarity 94.2%; Pred. No. 2e-49;
 Matches 146; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 278 MAAGSTTLPALPEDGGGAFPPGHHKDPKRLKCKNGGFLLRIHPDGRVDGKREKSDPH 337
 DB 1 MAAGSTTLPALPEDGGA-AFPFGHKKDKPKRLKCKNGGFLLRIHPDGRVDGKREKSDPH 59
 QY 338 KTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 397
 DB 60 KTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 119
 QY 398 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
 DB 120 TSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 154

RESULT 13
 FGF2_MONDO
 ID FGF2_MONDO STANDARD: PRT: 156 AA.

AC P48798;
 DT 01-FEB-1996 (rel. 33, last sequence update)
 DT 15-JUN-2002 (rel. 41, last annotation update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast
 DE growth factor) (BRGF) (Prostatoplkin).
 GN FGF2.
 OS Monodelphis domestica (Short-tailed grey opossum).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphins.
 CC NCBI_TaxID=13616;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=94296558; PubMed=8024698;
 RA Kuswilt D.F., Sabourin C.L.K., Sherburn T.E., Ley R.D.;
 RT "Characterization of cDNA encoding basic fibroblast growth factor of
 RT the marsupial Monodelphis domestica";
 RL DNA Cell Biol. 13:549-554(1994).
 CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
 CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
 CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
 CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES
 CC AFGF.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC -----
 DR EMBL: Z15154; CA78854.1; AL1_INIT.
 DR HSSP: P09038; 1BPF.
 DR InterPro: IPR002209; HB/F_growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HBGF_FGF_1.
 DR Growth factor; Mitogen; Angiogenesis; Heparin-binding.
 KW PROPEP 1 9
 FT CHAIN 1 156 HEPARIN-BINDING GROWTH FACTOR 2.
 FT BINDING 28 32 HEPARIN (POTENTIAL).
 FT BINDING 117 120 HEPARIN (POTENTIAL).
 FT BINDING 156 AA: 17303 MW: 7655FCC49BF1209 CRC64;
 SQ SEQUENCE

Query Match 31.5%; Score 754.5; DB 1; Length 156;
 Best Local Similarity 92.3%; Pred. No. 9.4e-48;
 Matches 144; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 278 MAAGSTTLPALPED-GGSAFPFGHHKDPKRLKCKNGGFLLRIHPDGRVDGKREKSDPH 336
 DB 1 MAAGSTTLPALSGDGGGAFPPGHHKDPKRLKCKNGGFLLRIHPDGRVDGKREKSDPH 60
 QY 337 IKTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 396
 DB 61 IKTLQLOAEERGVSIVKVCANRYLAKKEDGRLLASKCVTECEFFERLESNNNTYRSRK 120
 QY 397 YTSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 432
 DB 121 YTSMYVALKRTGOYKLGSKTGPQKAILFLPMSAAS 156

RESULT 14
 FGF2_CHICK
 ID FGF2_CHICK STANDARD: PRT: 158 AA.

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF).
 GN FGF2 OR FGF-2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246053; PubMed=7683281;
 RA Borth A.Z., Zeller R., Meijers C.;
 RT "Expression of alternatively spliced bFGF first coding exons and antisense mRNAs during chicken embryogenesis.";
 RL Dev. Biol. 157:110-118(1993).
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 CC EMBL: M95707; AAA48617.1; -
 CC HSSP: P09038; 1BFF.
 CC InterPro: IPR002209; HB/F-growthfact.
 CC InterPro: IPR002348; ILL_HBGF.
 CC Pfam: PF00167; FGF_1.
 CC PRINTS: PR00267; ILLHBGF.
 CC PRODOM: PD000831; HB/F-growthfact; 1.
 CC SMART: SM00442; FGF_1.
 CC PROSITE: PS00247; HBGF_FGF; 1.
 CC Growth factor; Mitogen; Angiogenesis; Heparin-binding.
 CC PROPEP
 CC FT CHAIN 1 12 BY SIMILARITY.
 CC FT BINDING 13 158 HEPARIN-BINDING GROWTH FACTOR 2.
 CC FT BINDING 30 34 HEPARIN (POTENTIAL).
 CC FT BINDING 119 122 HEPARIN (POTENTIAL).
 CC SEQUENCE 158 AA; 17374 MW; 7B69B684C17F1816 CRC64;
 Query Match 31.4%; Score 753; DB 1; Length 158;
 Best Local Similarity 91.6%; Pred. No. 1.2e-47;
 Matches 141; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 279 AASITTLPLPDPGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIK 338
 DB 5 AASITTLPLPDPGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIK 64
 QY 339 LQLOAERGVSIRKVCANRYLAKKEGRLIASCYDDECFEERLESNNYTRSKRYT 398
 DB 65 LQLOAERGVSIRKVCANRYLAKKEGRLIASCYDDECFEERLESNNYTRSKRYT 124
 QY 399 SWYVALKRTGQYKLGSKTGGOKAILFLPMSAAS 432
 DB 125 DWYVALKRTGQYKLGSKTGGOKAILFLPMSAAS 158
 RESULT 15
 FGF2_RABBIT
 ID FGF2_RABBIT STANDARD; PRT; 137 AA.
 AC P48799;
 DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heparin-binding growth factor 2 (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin) (Fragment).
 GN FGF2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Smooth muscle;
 RX MEDLINE=93343209; PubMed=8342599;
 RA Winkles J.A., Priesel R., Alberts G.F., Janat M.F., Liau G.;
 RT "Elevated expression of basic fibroblast growth factor in an immortalized rabbit smooth muscle cell line.";
 RL Am. J. Pathol. 143:518-527(1993).
 CC -1- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN DOES AFGF.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 CC EMBL: I12034; AAA31248.1; -
 CC HSSP: P09038; 1BFF.
 CC InterPro: IPR002209; HB/F-growthfact.
 CC Pfam: PF00167; FGF_1.
 CC PRODOM: PD000831; HB/F-growthfact; 1.
 CC SMART: SM00442; FGF_1.
 CC PROSITE: PS00247; HBGF_FGF; 1.
 CC Growth factor; Mitogen; Angiogenesis; Heparin-binding.
 CC KW BINDING 18 22 HEPARIN (POTENTIAL).
 CC FT BINDING 107 110 HEPARIN (POTENTIAL).
 CC FT NON_TER 137 137
 CC SQ SEQUENCE 137 AA; 15418 MW; 0D9BE457B88E8C51 CRC64;
 Query Match 30.8%; Score 738; DB 1; Length 137;
 Best Local Similarity 99.3%; Pred. No. 1.2e-46;
 Matches 136; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 287 PALPEGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIKLOAER 346
 DB 1 PALPEGGGAPPGPHFKDPKRLYCKNGGFLLRIHPDGVADVREKSDPHIKLOAER 60
 QY 347 GVVSTIGVCANRYLAKKEGRLIASCYDDECFEERLESNNYTRSKRYTSMVALKR 406
 DB 61 GVVSTIGVCANRYLAKKEGRLIASCYDDECFEERLESNNYTRSKRYTSMVALKR 120
 QY 407 TGOYKLGSKTGGOKAI 423
 DB 121 TGOYKLGSKTGGOKAI 137
 Search completed: March 13, 2003, 09:26:25
 Job time : 37 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 06:13:37 ; Search time 73 Seconds
(without alignments)
1289.911 Million cell updates/sec

Title: US-09-775-964-5
Perfect score: 2398
Sequence: 1 PTDLRFTNIGPDMRTVWAP.....LVTLPHNLMHGPETLDVPSY 457

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 824.5 | 34.4 | 196 | 4 P78443 | P78443 homo sapien |
| 2 | 762 | 31.8 | 153 | 6 Q925A3 | Q925A3 mus musculu |
| 3 | 760.5 | 31.7 | 2478 | 11 Q93406 | Q93406 brachydanio |
| 4 | 740.5 | 30.9 | 170 | 11 Q60487 | Q60487 cavia porce |
| 5 | 698 | 29.1 | 155 | 13 Q90Y92 | Q90Y92 cynops pyrr |
| 6 | 676 | 28.2 | 130 | 6 Q7767 | Q7767 cynops pyrr |
| 7 | 618 | 25.8 | 135 | 13 Q8QF9 | Q8QF9 canis famli |
| 8 | 585 | 24.4 | 111 | 6 Q9BDX1 | Q9BDX1 fugu rubrip |
| 9 | 561 | 23.4 | 108 | 6 Q9N1S7 | Q9N1S7 macaca mula |
| 10 | 561 | 23.4 | 125 | 13 Q98TP8 | Q98TP8 capreolus c |
| 11 | 484 | 20.2 | 109 | 11 Q925A1 | Q925A1 mus musculu |
| 12 | 480 | 20.0 | 112 | 11 Q925A2 | Q925A2 mus musculu |
| 13 | 476 | 19.8 | 101 | 13 P79706 | P79706 cynops pyrr |
| 14 | 474.5 | 19.8 | 146 | 13 Q07659 | Q07659 gallus gall |
| 15 | 457 | 19.1 | 87 | 6 Q8WMP4 | Q8WMP4 equus cabal |
| 16 | 428.5 | 17.9 | 379 | 4 Q95617 | Q95617 homo sapien |

| | | | | | |
|----|-------|------|------|-----------|--------------------|
| 17 | 417 | 17.4 | 293 | 6 Q9XSG0 | Q9XSG0 oryctolagus |
| 18 | 415.5 | 17.3 | 810 | 11 Q8R3F3 | Q8R3F3 mus musculu |
| 19 | 394 | 16.4 | 712 | 4 Q00531 | Q00531 homo sapien |
| 20 | 394 | 16.4 | 4 | Q92752 | Q92752 homo sapien |
| 21 | 394 | 16.4 | 4 | Q15568 | Q15568 homo sapien |
| 22 | 383.5 | 16.0 | 354 | 4 Q9UQ56 | Q9UQ56 homo sapien |
| 23 | 378.5 | 15.8 | 1356 | 11 Q05546 | Q05546 rattus norv |
| 24 | 358 | 14.9 | 1353 | 13 Q00546 | Q00546 rattus norv |
| 25 | 341 | 14.2 | 76 | 6 Q9N0V2 | Q9N0V2 ovis aries |
| 26 | 336 | 14.0 | 1532 | 13 Q90994 | Q90994 gallus gall |
| 27 | 332.5 | 13.9 | 114 | 4 Q16443 | Q16443 homo sapien |
| 28 | 332.5 | 13.9 | 114 | 4 Q00527 | Q00527 homo sapien |
| 29 | 329 | 13.7 | 1810 | 13 Q90824 | Q90824 gallus gall |
| 30 | 327 | 13.6 | 2019 | 11 Q64706 | Q64706 mus musculu |
| 31 | 326.5 | 13.6 | 614 | 13 Q90484 | Q90484 brachydanio |
| 32 | 325 | 13.6 | 1294 | 4 Q9UQ53 | Q9UQ53 homo sapien |
| 33 | 323.5 | 13.5 | 592 | 4 Q95697 | Q95697 homo sapien |
| 34 | 318 | 13.3 | 619 | 11 Q62701 | Q62701 rattus norv |
| 35 | 317 | 13.2 | 1714 | 13 Q90995 | Q90995 gallus gall |
| 36 | 312.5 | 13.0 | 922 | 13 Q93405 | Q93405 brachydanio |
| 37 | 309 | 12.9 | 654 | 4 Q00210 | Q00210 homo sapien |
| 38 | 308.5 | 12.9 | 347 | 4 Q96KP9 | Q96KP9 homo sapien |
| 39 | 306.5 | 12.8 | 347 | 6 Q95KV5 | Q95KV5 bos taurus |
| 40 | 305 | 12.7 | 68 | 6 Q28692 | Q28692 oryctolagus |
| 41 | 302.5 | 12.6 | 4135 | 6 Q18977 | Q18977 bos taurus |
| 42 | 301 | 12.6 | 272 | 4 Q9H1P7 | Q9H1P7 homo sapien |
| 43 | 299 | 12.5 | 672 | 4 Q60782 | Q60782 homo sapien |
| 44 | 297.5 | 12.4 | 843 | 4 Q05707 | Q05707 homo sapien |
| 45 | 292 | 12.2 | 106 | 6 Q9N1S8 | Q9N1S8 capreolus c |

ALIGNMENTS

RESULT 1

P78443 PRELIMINARY: PRT: 196 AA.

AC P78443: 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE 21 kDa basic fibroblast growth factor (BFGF).

GN BFGF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP MEDLINE-69184522; PubMed-2538817;

RX Piatz H., Kagnad M., Piatz A.C., Klagsbrun M., Lelias J.M., Liauzun P., Chalou P., Tauber J.P., Amalric F., Smith J.A., Caput D.; "High molecular mass forms of basic fibroblast growth factor are initiated by alternative CUG codons.";

RT Proc. Natl. Acad. Sci. U.S.A. 86:1836-1840(1989).

RL [2]

RN SEQUENCE OF 81-168 FROM N.A.

RP MEDLINE-93038590; PubMed-1417798;

RX Watson R., Anthony F., Pickett M., Lambden P., Masson G.M., Thomas E.J.; "Reverse transcription with nested polymerase chain reaction shows expression of basic fibroblast growth factor transcripts in human granulosa and cumulus cells from in vitro fertilisation patients.";

RT Biochem. Biophys. Res. Commun. 187:1227-1231(1992).

DR EMBL: J04513; AAA52532.1; -;

DR EMBL: S47380; AAD13853.1; -;

DR HSSP: P09038; 1BFF.

DR InterPro: IPR002209; HB/F-growthfact.

DR InterPro: IPR002348; IL1_HBGF.

DR Pfam: PF00167; FGF_1.

DR PRINTS: PR00262; IL1HBGF.

DR Prodom: PD000831; HB/F-growthfact; 1.

DR SMART: SM00442; FGF_1.

DR PROSITE; PS00247; HBGF_FGF; 1.
 SQ SEQUENCE 196 AA; 21203 MW; D6B5447137560343 CRC64;
 Query Match 34.4%; Score 824.5; DB 4; Length 196;
 Best Local Similarity 88.8%; Pred. No. 4.5e-54;
 Matches 159; Conservative 4; Mismatches 15; Indels 1; Gaps 1;

QY 254 GRGSPASSKPSISINYTEIDKPSMAGSITTLPALPEDGSGGAFPPGHFKDPKRLCKN 313
 19 GRGTAAPRAAPAAAGSRG-PAGMAGSITTLPALPEDGSGGAFPPGHFKDPKRLCKN 77
 DB 314 GGFRLRHPPDGRVGRKSPHKLQLOAEERGVSITGVCANRYLAMKEDGRLASKC 373
 78 GGFRLRHPPDGRVGRKSPHKLQLOAEERGVSITGVCANRYLAMKEDGRLASKC 137
 QY 374 VTDECFEERLESNNYTRSRKRTSVYVALKRTGQYKLGSKTGPGKAILFLPMSAAS 432
 138 VTDECFEERLESNNYTRSRKRTSVYVALKRTGQYKLGSKTGPGKAILFLPMSAAS 196

OUT 2
 ID 0925A3 PRELIMINARY; PRT; 153 AA.
 AC 0925A3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Fibroblast growth factor 2.
 GN FGF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N.
 RA Dicks R.P., Griep A.E.;
 RT "Multiple novel variants of fibroblast growth factor 2 transcripts are
 expressed in mouse embryos."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY027551; AAK52308.1;
 DR InterPro; IPR002209; HB/F-growthfact.
 DR Pfam; PF00167; FGF; 1.
 DR ProDom; PD000831; HB/F-growthfact; 1.
 SQ SEQUENCE 153 AA; 17024 MW; AD8163CD8FA2FAAB CRC64;

Query Match 31.8%; Score 762; DB 11; Length 153;
 Best Local Similarity 93.5%; Pred. No. 1.5e-49;
 Matches 145; Conservative 5; Mismatches 3; Indels 2; Gaps 2;

QY 278 MAAGSITTLPALPEDGSGGAFPPGHFKDPKRLCKNGGFLRIHPDGRVGRKSPH 337
 1 MAAGSITSLPALPEDGGA-APPPGHFKDPKRLCKNGGFLRIHPDGRVGRKSPH 59
 DB 338 KLOLOAERGVSITGVCANRYLAMKEDGRLASKCVTDECFEERLESNNYTRSRKY 397
 60 KLOLOAERGVSITGVCANRYLAMKEDGRLAS-CVTECFEERLESNNYTRSRKY 118
 QY 398 TSWYVALKRTGQYKLGSKTGPGKAILFLPMSAAS 432
 119 SSWYVALKRTGQYKLGSKTGPGKAILFLPMSAKS 153

RESULT 3
 ID 093406 PRELIMINARY; PRT; 2478 AA.
 AC 093406;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Fibronectin.
 GN FN1.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhao Q., Colliodi P.;
 RT "Characterization and expression of zebrafish fibronectin."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF081128; ARC31947.1;
 DR FGF2.
 DR ZFIN; ZDB-GENE-000426-1; fn1.
 DR InterPro; IPR00361; EGF-like.
 DR InterPro; IPR000083; Fibrncn1.
 DR InterPro; IPR003962; fn11-repeat.
 DR InterPro; IPR003961; fn11.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00039; fn1; 12.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF00041; fn3; 17.
 DR PRINTS; PRO0012; ENTYPET.
 DR PRINTS; PRO0013; ENTYPETII.
 DR PRINTS; PRO0014; ENTYPETII.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SM00058; FN1; 12.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00060; FN3; 14.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01253; FIBRONECTIN_1; UNKNOWN_11.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 KW Repeat.
 SQ SEQUENCE 2478 AA; 271652 MW; A03475C55A385750 CRC64;

Query Match 31.7%; Score 760.5; DB 13; Length 2478;
 Best Local Similarity 54.3%; Pred. No. 9.8e-48;
 Matches 152; Conservative 45; Mismatches 78; Indels 5; Gaps 4;

QY 1 PDLRFTNIGCPDRTMTW-AF--PPSIDLTNPLRVSPVKNEDVAELISPSDNAVLT 57
 1359 PDLSTGEVYADMLVTKWAKPVKSSDINOYIRHPVDEDEDETFERTVEGSENVVL 1418
 DB 58 NLPGREYVSVSSVYEOHESPLRGKRGKTDSPGIDFSDITANSFVHIAARAT 117
 1419 HLPNREYLVSVYEGRESGALGPRLFL-MPCCLGFSVDVGTSTFVRWQARATIS 1477
 QY 118 GYRIIRHHPHESRPREDVPHSRNSITLTNLTGREGYVSIALNGRESPLIGQOST 177
 1478 GYRIIRHHPHESRPREDVPHSRNSITLTNLTGREGYVSIALNGRESPLIGQOST 1536
 DB 178 VSDVPDLEEVAAPTSLISMDAPAVTVYRYRTYGETGNSPVOELTPGSKSTATIS 237
 1537 ISDAPDLEVISSTPSISVIRMDAPSVTVYRYRTYGETGNSGSDAPLEFWPGSSTATIE 1596
 QY 238 GLKPGVDYITVYAVTGRGSDSPASSKPSISINRTEIDKPS 277
 1597 DLRPGETYITVYAVTGRGSDSPASSKPSIHKRTIDSPS 1636

RESULT 4
 ID 060487 PRELIMINARY; PRT; 170 AA.
 AC 060487;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Fibroblast growth factor 2 (FGF-2) (Fibroblast growth factor, basic)
 DE (bFGF) (Heparin-binding growth factor 2) (HBGF-2) (Prostatropin)
 DE (Prostatic growth factor) (Fragments).
 GN FGF2.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;

RN [1] SEQUENCE OF 53-170 FROM N.A.
 RP TISSUE-PROSTATE;
 RA Ricciardelli C.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF N-TERMINUS, PARTIAL SEQUENCE, AND ALTERNATIVE SPLICING.
 RX MEDLINE=89273588; PubMed=2730645;
 RA Sommer A., Moscattelli D., Rifkin D.B.;
 RT "An amino-terminally extended and post-translationally modified form
 of a 25KD basic fibroblast growth factor.";
 RL Biochem. Biophys. Res. Commun. 160:1267-1274(1989).
 RN [3]
 RP PARTIAL SEQUENCE, AND METHYLATION.
 RX MEDLINE=91322114; PubMed=1713785;
 RA Burgess W.H., Bizik J., Mehlman J., Quarto N., Rifkin D.B.;
 RT "Direct evidence for methylation of arginine residues in high
 molecular weight forms of basic fibroblast growth factor.";
 RL Cell Regul. 2:87-93(1991).
 RN [4]
 RP CHARACTERIZATION.
 RX TISSUE-BRAIN;
 RX MEDLINE=87289686; PubMed=3475702;
 RA Moscattelli D., Joseph-Silverstein J., Manojas R., Rifkin D.B.;
 RT "Mr 25,000 heparin-binding protein from guinea pig brain is a high
 molecular weight form of basic fibroblast growth factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5778-5782(1987).
 CC -1- FUNCTION: WIDE-SPECTRUM MITOGENIC, ANGIOGENIC, AND NEUROTROPHIC
 FACTOR. IMPLICATED IN A MULTITUDE OF PHYSIOLOGIC AND PATHOLOGIC
 PROCESSES, INCLUDING LIMB DEVELOPMENT, ANGIOGENESIS, WOUND
 HEALING, AND TUMOR GROWTH. POTENT MITOGEN AND CHEMOATTRACTANT FOR
 MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION,
 PROLIFERATION, AND MAINTENANCE OF CELLS IN THE CENTRAL NERVOUS
 SYSTEM AND IN BONE FORMATION. MAJOR ANGIOGENIC FACTOR THAT ALSO
 ACTIVATES TUMOR NEOVASCULARIZATION (BY SIMILARITY).
 CC -1- SUBUNIT: FORMS A QUATERNARY COMPLEX WITH TWO FGFR1 AND AT LEAST
 ONE HEPARAN SULFATE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST TWO ISOFORMS: 18 KDA AND 25 KDA
 (SHOWN HERE); MAY BE PRODUCED BY USE OF ALTERNATIVE TRANSLATION
 INITIATION SITES. BOTH FORMS ARE ACTIVE.
 CC -1- PTM: THE N-TERMINAL OF ISOFORM 18 KDA IS BLOCKED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; MANY FRAMESHIFTS WERE
 INTRODUCED FROM RESIDUES 77, 88, 93 AND 149 DOWNWARD TO EXTEND THE
 SIMILARITY TO THE HUMAN SEQUENCE AS WELL AS ON THE BASIS OF
 PARTIAL AMINO-ACID SEQUENCING.
 CC EMBL: L75974; AAA85394.1; ALT_FRAME.
 DR HSSP; P09038; BLA.
 DR InterPro: IPR002209; HB/F_growthfact.
 DR InterPro: IPR002348; IL1_HBGF.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KW Growth factor; Mitogen; Vascularization; Heparin-binding;
 KW Alternative initiation; Methylation; Phosphorylation;
 KW Developmental protein.
 FT NON_TER 1
 FT NON_CONS 15
 FT CHAIN <1 170 25 KDA BASIC FIBROBLAST GROWTH FACTOR.
 FT CHAIN 22 170 18 KDA BASIC FIBROBLAST GROWTH FACTOR.
 FT INT_MET 22 22 FOR 18 KDA FORM.
 FT DOMAIN 11 14 POLY-ALA.
 FT NON_CONS 50 51
 FT SITE 61 63
 FT SITE 103 105 CELL ATTACHMENT SITE (POTENTIAL).
 FT BINDING 50 51 CELL ATTACHMENT SITE (POTENTIAL).
 FT BINDING 105 105 HEPARIN (BY SIMILARITY).
 FT BINDING 143 159 HEPARIN (BY SIMILARITY).
 FT MOD_RES 4 4 METHYLATION (MONO- OR DI-).
 FT MOD_RES 6 6 METHYLATION (MONO- OR DI-).
 FT MOD_RES 8 8 METHYLATION (MONO- OR DI-).
 FT MOD_RES 88 88 PHOSPHORYLATION (BY SIMILARITY).

FT MOD_RES 136 136 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 170 AA: 18354 MW: F36BDBC736E5FEBC CRC64;
 Query Match 30.9%; Score 740.5; DB 11; Length 170;
 Best Local Similarity 80.7%; Pred. No. 7.2e-48;
 Matches 146; Conservative 8; Mismatches 8; Indels 19; Gaps 3;
 QY 254 GGGDSASSKPSINRTFIDKP--SMAGSTTTTPALPEGDSGAFPGGHRKDPRLIC 311
 DB 7 GGTATAAARR-----EPGGAMAAGSTTTTPALPEGDSGAFAPGHRKP----- 50
 QY 312 KNGGFLRLHPDGRVDGVRKESDPHTKLOLAEEGRVSIKGCARLYLAMEDEGLLAS 371
 DB 51 -NGGFLRLHPDGRVDGVRKEDTPHTKLOLAEDRGVSIKGCARLYLAMEDEGLLAS 109
 QY 372 KCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGYKLGSKTGPQKAILFLPMSAA 431
 DB 110 KCVTDECFEERLESNNNTYRSRKYTSWYVALKRTGYKLGSKTGPQKAILFLPMSAK 169
 QY 432 S 432
 DB 170 S 170
 RESULT 5
 ID Q90Y92 PRELIMINARY; PRT; 155 AA.
 AC Q90Y92;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Fibroblast growth factor-2.
 GN FGF-2.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Susaki K., Nakamura K., Chiba C., Saito T.;
 RT "Expression of FGF2 during newt retinal development and
 regeneration.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB064664; BAB63249.1; -
 DR InterPro: IPR002209; HB/F_growthfact.
 DR Pfam; PF00167; FGF; 1.
 DR ProDom: PD000831; HB/F_growthfact; 1.
 DR PROSITE; PS00247; HBGF_FGF; UNKNOWN.1.
 SO SEQUENCE 155 AA: 17278 MW: 28583058538AB8D9 CRC64;
 Query Match 29.1%; Score 698; DB 13; Length 155;
 Best Local Similarity 85.2%; Pred. No. 9.5e-45;
 Matches 132; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
 QY 278 MAGSTTTTPALPEGDSGAFPGGHRKDPRLIC 337
 DB 1 MAGSTTTTPALPEGDSGAFPGGHRKDPRLIC 60
 QY 338 KLOLAEEGRVSIKGCARLYLAMEDEGLLAS 397
 DB 61 KLOLAEEGRVSIKGCARLYLAMEDEGLLAS 120
 QY 398 TSMYVALKRTGYKLGSKTGPQKAILFLPMSAA 432
 DB 121 SDMYVALKRTGYKLGSKTGPQKAILFLPMSAKS 155
 RESULT 6
 ID Q77767 PRELIMINARY; PRT; 130 AA.
 AC Q77767;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)

01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Basic fibroblast growth factor (bFGF) (FGF-2) (Heparin-binding growth factor 2) (HMGF-2) (Prostatoplin) (Prostatic growth factor) (Fragment).
 DE bFGF.
 GN Canis familiaris (dog).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ADRENAL GLAND;
 RA Trochta O.A., Jacobs R.M., Lamarre J.;
 RT "The role of bFGF in canine Hemangiosarcoma";
 RL Submitted (Apr-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: WIDE-SPECTRUM MITOGENIC, ANGIOGENIC, AND NEUROTROPHIC FACTOR. IMPLICATED IN A MULTITUDE OF PHYSIOLOGIC AND PATHOLOGIC PROCESSES, INCLUDING LIMB DEVELOPMENT, ANGIOGENESIS, WOUND HEALING, AND TUMOR GROWTH. POTENT MITOGEN AND CHEMOATTRACTANT FOR MESENCHYME-DERIVED CELLS. IMPLICATED IN THE DIFFERENTIATION, PROLIFERATION, AND MAINTENANCE OF CELLS IN THE CENTRAL NERVOUS SYSTEM AND IN BONE VASCULARIZATION. MAJOR ANGIOGENIC FACTOR THAT ALSO ACTIVATES TUMOR NEOVASCULARIZATION (BY SIMILARITY).
 CC -1- SUBUNIT: FORMS A QUATERNARY COMPLEX WITH TWO FGFR1 AND AT LEAST ONE HEPARAN SULFATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 DR EMBL: AF060562; AAC35912.1; -.
 DR HSSP: P09038; 1BFF.
 DR InterPro: IPR002209; HB/F_growthfact.
 DR InterPro: IPR002348; ILL_HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; ILLHBGF.
 DR PRODOM: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 KW Growth factor; Mitogen; Vascularization; Heparin-binding; Phosphorylation; Developmental protein.
 FT NON_TER 1
 FT SITE 21 23
 FT BINDING 63 65
 FT BINDING 10 11
 FT BINDING 65 65
 FT BINDING 103 119
 FT MOD_RES 48 48
 FT MOD_RES 96 96
 FT NON_TER 130
 FT SEQUENCE 130 AA; 14902 MW; 21900876E878FAEA CRC64;
 Query Match 28.2%; Score 676; DB 6; Length 130;
 Best Local Similarity 96.9%; Pred. No. 3,3e-43;
 Matches 126; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 303 FKDPRLCKNGGFLRLHPDGRVGVREKSPHKLKLOLAEEGRVSVISGVCANRYLAM 362
 DB 1 FKDPRLCKNGGFLRLHPDGRVGVREKSPHKLKLOLAEEGRVSVISGVCANRYLAM 60
 OY 363 KEDGRLASCVTDCEPPEERLESNNYNTYRSKRTSWYVALKRGQYKLKSGPGOKA 422
 DB 61 KEDGRLASCVTDCEPPEERLESNNYNTYRSKRTSWYVALKRGQYKLKSGPGOKA 120
 OY 423 ILFLPMSAAS 432
 DB 121 ILFLPMSAKS 130
 RESULT 7
 Q8QFR9 PRELIMINARY; PRT; 155 AA.
 AC Q8QFR9;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Basic fibroblast growth factor.

FGF2.
 OS Eury rubripes (Japanese pufferfish) (Takifugu rubripes).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CC Tetraodontidae; Takifugu.
 NCBI_TaxID=31033;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Botchenby M.R.;
 RT "Comparative vertebrate genomic sequence analysis studies based on Fugu rubripes";
 RL Thesis (2001), University College London, London, United Kingdom.
 DR EMBL: AJ426040; CAD19830.1; -.
 SO SEQUENCE 155 AA; 17113 MW; AEFEL2DBDC78FBBE CRC64;
 Query Match 25.8%; Score 618; DB 13; Length 155;
 Best Local Similarity 77.1%; Pred. No. 9,2e-39;
 Matches 118; Conservative 5; Mismatches 30; Indels 0; Gaps 0;
 OY 278 MAAGSITLPLAPEDGGGAPPPGHFKDPKRLYCKNGGFLRLHPDGVGVREKSDPHI 337
 DB 1 MATGGITLPLTPEDDGGSGGPPGSKDPKRLYCKNGGFLRLSDGAVDGTREKTDPHI 60
 OY 338 KLOLAEEGRVSVISGVCANRYLAMKEDGRLASCVTDCEPPEERLESNNYNTYRSRY 397
 DB 61 KLOLAATSVGEVYIKGVCANRYLAMNRDGRILFGMKRAIDECHFLERLESNNYNTYRSRY 120
 OY 398 TSWYVALKRGQYKLKSGTGPQOKAILFLPMSA 430
 DB 121 PMFVGLTRTGTNGYKSGITGPGOKAILFLPMSA 153
 RESULT 8
 Q9BDX1 PRELIMINARY; PRT; 111 AA.
 AC Q9BDX1;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Basic fibroblast growth factor (Fragment).
 OS Macaca mulatta (Rhesus macaque).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sekhon H.S., Keller J.R., Spindel E.R.;
 RT "Alterations in Collagen and Elastin Gene Expression in Fetal Pulmonary Vessels in Monkeys Following Prenatal Nicotine Exposure: A Possible Role of alpha7 Nicotinic Acetylcholine Receptor in Persistent Pulmonary Hypertension";
 RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF251270; AAK37962.1; -.
 DR HSSP: P09038; 2EGF.
 DR InterPro: IPR002209; HB/F_growthfact.
 DR InterPro: IPR002348; ILL_HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; ILLHBGF.
 DR PRODOM: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 FT NON_TER 1
 FT NON_TER 111
 FT SEQUENCE 111 AA; 12633 MW; EC0967A5261F5487 CRC64;
 Query Match 24.4%; Score 585; DB 6; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1,7e-36;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 320 IHPDGRVGVREKSPHKLKLOLAEEGRVSVISGVCANRYLAMKEDGRLASCVTDCEP 379
 IHPDGRVGVREKSPHKLKLOLAEEGRVSVISGVCANRYLAMKEDGRLASCVTDCEP 379

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Db 1 IHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLLASCKVTDGC 60
OY 380 FFERLESNNYNTYRSRKYTSWYVALKRTGYKSGTGPGOKAILFLPMSA 430
    |||||||
Db 61 FFERLESNNYNTYRSRKYTSWYVALKRTGYKSGTGPGOKAILFLPMSA 111

RESULT 9
OY 9N1S7 PRELIMINARY: PRT: 108 AA.
AC 09N1S7:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Basic fibroblast growth factor (Fragment).
CN BFGF.
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Capreolus.
NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=20532861; PubMed=11078967;
RA Wagener A., Biotner S., Goritz F., Fickel J.;
RT "Detection of growth factors in the testis of roe deer (Capreolus
RT capreolus).";
RL Annu. Reprod. Sci. 64:65-75(2000).
DR EMBL: AF152587; AAF73226.1; -.
DR HSSP: P09038; 4FGF.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12399 MW; 6BC7B7244214567E CRC64;

Query Match
Best Local Similarity 23.4%; Score 561; DB 6; Length 108;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 319 RIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLLASCKVTDGC 378
    |||||||
b 1 RIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLLASCKVTDGC 60
OY 379 FFERLESNNYNTYRSRKYTSWYVALKRTGYKSGTGPGOKAILFL 426
    |||||||
Db 61 FFERLESNNYNTYRSRKYTSWYVALKRTGYKSGTGPGOKAILFL 108

RESULT 10
OY 9N1S7 PRELIMINARY: PRT: 125 AA.
AC 09N1S7:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor-2 (Fragment).
CN FGF-2.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno N., Hayashi T., Kondoh H., Okamoto M.;
RT "Cynops fibroblast growth factor-2.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AB049625; BAB40835.1; -.
DR HSSP: P09038; 1BFP.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 125 AA; 14244 MW; 5C27F41DC6E60C13 CRC64;

Query Match
Best Local Similarity 23.4%; Score 561; DB 13; Length 125;
Matches 107; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

OY 309 LYCKNGGFRLRIHPDGRVGVREKSDPHIKLQQAEEGVVSIGVCANRYLAMKEDGRLL 368
    |||||||
Db 2 LYCKNGGFRLRINSKGVKQVQAREKSDSYIKLQQAEEGVVSIGVCANRYLAMKEDGRLL 61
OY 369 LASKCVTDGCFPERLESNNYNTYRSRKYTSWYVALKRTGYKSGTGPGOKAILFLPM 428
    |||||||
Db 62 MALKWITDGCFFPERLESNNYNTYRSRKYTSWYVALKRTGYKSGTGAGOKAILFLPM 121
OY 429 SAAS 432
    |||
Db 122 SAAS 125

RESULT 11
OY 9N25A1 PRELIMINARY: PRT: 109 AA.
AC 0925A1:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Fibroblast growth factor 2.
CN FGF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Dirks R.P., Gilep A.E.;
RT "Multiple novel variants of fibroblast growth factor 2 transcripts are
RT expressed in mouse embryos.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY027558; AAK52310.1; -.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR PROSITE: PS00247; HBGF_FGF; UNKNOW1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12388 MW; 61074ADE3303C860 CRC64;

Query Match
Best Local Similarity 20.2%; Score 484; DB 11; Length 109;
Matches 93; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 337 IKLQQAEEGVVSIGVCANRYLAMKEDGRLLASCKVTDGCFPERLESNNYNTYRSRK 396
    |||||||
Db 14 IKLQQAEEGVVSIGVCANRYLAMKEDGRLLASCKVTDGCFPERLESNNYNTYRSRK 73
OY 397 YTSWYVALKRTGYKSGTGPGOKAILFLPMSAAS 432
    |||||||
Db 74 YTSWYVALKRTGYKSGTGPGOKAILFLPMSAKS 109

RESULT 12
OY 9N25A2

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ID Q925A2 PRELIMINARY; PRT: 112 AA.
 AC Q925A2:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fibroblast growth factor 2.
 GN FGF2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Dicks R.P., Griep A.E.;
 RT "Multiple novel variants of fibroblast growth factor 2 transcripts are
 expressed in mouse embryos."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1021537; AAK52309.1;
 DR InterPro: IPR002209; HB/F-growthfact.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F-growthfact; 1.
 DR PROSITE: PS00247; HBGF_FGF; UNKNOWN_1.
 SQ SEQUENCE 112 AA: 12725 MW: 800557ABE0257CCB CRC64:

Query Match 20.0%; Score 480; DB 11; Length 112;
 Best Local Similarity 96.8%; Pred. No. 1.2e-28;
 Matches 92; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 338 KIOLOEEGVGVSIKVCANRYIAMKEDGRLLASKCVTECFEFLSENNNTYRSRY 397
 DB 18 KIOLOEEGVGVSIKVCANRYIAMKEDGRLLASKCVTECFEFLSENNNTYRSRY 77
 QY 398 TSMYVALKRTGQYKLSKGTGPGOKALFLPMSAAS 432
 DB 78 TSMYVALKRTGQYKLSKGTGPGOKALFLPMSAAS 112

RESULT 13
 ID P79706 PRELIMINARY; PRT: 101 AA.
 AC P79706:
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Basic FGF (Fragment).
 GN Cynops pyrrhogaster (Japanese common newt).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EMBRYO;
 RA Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takashima K.,
 Kaneda T.;
 RT "Serial expression of the genes in a mesodermalizing ectoderms of
 early Cynops gastrula."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D89443; BAA13958.1;
 DR HSSP: P09038; 4RGE.
 DR InterPro: IPR002209; HB/F-growthfact.
 DR InterPro: IPR002348; IL1HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F-growthfact; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 FT NON_TER 1
 SQ SEQUENCE 101 AA: 11907 MW: 74A16C866C1F457A CRC64:

Query Match 19.8%; Score 476; DB 13; Length 101;
 Best Local Similarity 87.1%; Pred. No. 2.1e-28;
 Matches 88; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 306 PKRLCKNGCFELRIHPDGVGVREKSPHRIKLOLAEEGVGVSIKVCANRYIAMKED 365
 DB 1 PKRLCKNGCFELRIHPDGVGVREKSPHRIKLOLAEEGVGVSIKVCANRYIAMKED 60
 QY 366 GRLLASKCVTDECFEFLSENNNTYRSRYTSWYVALKR 406
 DB 61 GRLLASKCVTDECFEFLSENNNTYRSRYTSWYVALKR 101

RESULT 14
 ID Q07659 PRELIMINARY; PRT: 146 AA.
 AC Q07659:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Fibroblast growth factor.
 GN BFGF.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93246053; PubMed=7683281;
 RA Bria A.Z., Zeller R., Weijers G.;
 RT "Expression of alternatively spliced bfgf first coding exons and
 antisense mRNAs during chicken embryogenesis."
 RL Dev. Biol. 157:110-118(1993).
 RN [2]
 RP SEQUENCE OF 52-85 FROM N.A.
 RX MEDLINE=90382254; PubMed=2401202;
 RA Mitrani E., Gruenbaum Y., Shohat H., Ziv T.;
 RT "Fibroblast growth factor during mesoderm induction in the early chick
 embryo."
 RL Development 109:387-393(1990).
 DR EMBL: M95706; AAA48616.1;
 DR EMBL: X56804; CAA40139.1;
 DR HSSP: P09038; 2BPH.
 DR InterPro: IPR002209; HB/F-growthfact.
 DR InterPro: IPR002348; IL1HBGF.
 DR Pfam: PF00167; FGF_1.
 DR PRINTS: PR00262; IL1HBGF.
 DR ProDom: PD000831; HB/F-growthfact; 1.
 DR SMART: SM00442; FGF_1.
 DR PROSITE: PS00247; HBGF_FGF; 1.
 SQ SEQUENCE 146 AA: 16182 MW: A7CB97BCB456E247 CRC64:

Query Match 19.8%; Score 474.5; DB 13; Length 146;
 Best Local Similarity 58.4%; Pred. No. 4.6e-28;
 Matches 101; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

QY 260 ASSKPSIWKREIDKPSMAAGSTITLPAIPEDGSGAEPFGHFKDPKRLYCKNGCFELR 319
 DB 5 ASSQPRG---TAVGAPRVMSPPADVPSPSLPDGV-----LWER 40
 QY 320 IHPDGVGVREKSPHRIKLOLAEEGVGVSIKVCANRYIAMKEDGRLLASKCVTDECF 379
 DB 41 VHPDERVSAM-----VKLOLAEEGVGVSIKVCANRYIAMKEDGRLLASKCVTDECF 93
 QY 380 FFERLESNNNTYRSRYTSWYVALKRTGQYKLSKGTGPGOKALFLPMSAAS 432
 DB 94 FFERLESNNNTYRSRYTSWYVALKRTGQYKPGKGTGPGOKALFLPMSAAS 146

RESULT 15
 ID Q8WMP4 PRELIMINARY; PRT: 87 AA.
 Q8WMP4

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AC Q8MMP4;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)
DE Fibroblast growth factor 2 (Fragment).
GN FGF2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RA Einspanier R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RA Welter H.;
RL Thesis (2002), Department of Physiology, University of Munich,
  Freising, Germany.
DR EMBL: AJ319906; CAC86028.1;
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF_1.
DR PRINTS: PR00262; IL1HBGF.
DR PRODOM: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 87 AA; 10128 MW; 52382DDF0245739E CRC64;

Query Match          19.1%; Score 457; DB 6; Length 87;
Best Local Similarity 98.9%; Pred. No. 4.6e-27;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 318 LRIHPGKRVGVREKSDPHIKLOLAERGVSIKGVCANRYLAMKEDGRLLASKCVTDE 377
DB 1 LRIHPGKRVGVREKSDPHIKLOLAERGVSIKGVCANRYLAMKEDGRLLASKCVTDE 60

OY 378 CFFERLESNNNTYRSRKYTSWYVAL 404
DB 61 CFFERLESNNNTYRSRKYTSWYVAL 87

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 Job time : 81 secs

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